

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 2, 2006, 18:41:26 ; Search time 70.0319 Seconds
(without alignments)
1530.851 Million cell updates/sec

Title: US-10-088-703A-2

Perfect score: 1238
Sequence: 1 MDTESRRANLALPOEPSSV.....YGSATYSELDPGEMSPIDL 244

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1238	100.0	244	2 AAW75918	Aaw75918 Human bet
2	1238	100.0	244	4 AAB72900	Aab72900 Human IGE
3	1238	100.0	244	4 AAB74447	Aab74447 Human wil
4	1238	100.0	244	5 ABP65043	Abp65043 Human mem
5	1238	100.0	244	5 AAU88021	Aau88021 Human IGE
6	1238	100.0	244	8 ADQ90468	Adq90468 Human IGE
7	1231	99.4	244	4 AAW29149	Aaw29149 Human hig
8	910	73.5	195	4 AAB74448	Aab74448 Human var
9	697.5	56.3	235	5 ABP65047	Abp65047 Mouse mem
10	697.5	56.3	235	5 AAU88020	Aau88020 Mouse IGE
11	697.5	56.3	235	8 ADQ90467	Adq90467 Mouse IGE
12	645.5	52.1	243	2 AAR42341	Aar42341 Subunit o
13	645.5	52.1	243	5 ABP65048	Abp65048 Rat membr
14	645.5	52.1	246	2 AAR14770	Aar14770 Beta subu
15	645.5	52.1	246	2 AAR42337	Aar42337 Human Pce
16	636.5	51.4	243	2 AAR05026	Aar05026 Beta subu
17	283	22.9	112	2 AAR05027	Aar05027 Deleted f
18	283	22.9	115	2 AAR14771	Aar14771 Truncated
19	210	17.0	244	4 AAG63825	Aag63825 Immunoglo
20	209	16.9	244	5 ABP65036	Abp65036 Mouse mem
21	201.5	16.3	247	5 ABP65038	Abp65038 Mouse mem
22	200.5	16.2	247	4 AAE05353	Aae05353 Mouse hig
23	200.5	16.2	247	5 ABB72363	Abb72363 Murine pr
24	196	15.8	268	5 ABP65040	Abp65040 Mouse mem

25	191	15.4	197	7	ADN39134	Adn39134 Cancer/an
26	190	15.3	220	5	ABP90317	Abp90317 Human pol
27	190	15.3	220	5	ABP65023	Abp65023 Human mem
28	190	15.3	220	6	ABP55608	Abp55608 Amino aci
29	190	15.3	220	7	ADN39992	Adn39992 Cancer/an
30	190	15.3	220	8	ADP25105	Adp25105 PRO polyp
31	190	15.3	220	8	ADU06669	Adu06669 Novel bro
32	190	15.3	239	2	AAW96745	Aaw96745 High affi
33	190	15.3	239	3	AAV50174	Aav50174 Human hig
34	190	15.3	239	7	ADK65835	Adk65835 Angiogene
35	190	15.3	245	3	AAV94973	Aav94973 Human sec
36	190	15.3	246	5	ADR41417	Adr41417 Human CD-
37	189.5	15.3	267	2	AAV15224	Aav15224 Human rec
38	189.5	15.3	267	6	ADA10964	Ada10964 Human cdn
39	189.5	15.3	273	4	ABG17004	Abg17004 Novel hum
40	189.5	15.3	299	3	AAV91352	Aav91352 Human sec
41	189.5	15.3	308	5	ADR41397	Adr41397 Human CD-
42	188	15.2	231	5	ADR41416	Adr41416 Human CD-
43	186.5	15.1	214	6	ADA83822	Ada83822 Human MS4
44	186	15.0	267	5	ABP65045	Abp65045 Human mem
45	186	15.0	267	7	ADD13125	Add13125 Human MS4

ALIGNMENTS

RESULT 1

AAW75918
ID AAW75918 standard; protein; 244 AA.

AC AAW75918;

DT 13-NOV-1998 (first entry)

DE Human beta subunit of Fc epsilon RI polypeptide sequence.

KW Human beta subunit of Fc epsilon RI; ARAM; Fc epsilon RI beta chain;

KW antigen recognition activation motif; human beta subunit; allergy;

KW high-affinity immunoglobulin E receptor.

OS Homo sapiens.

Key Location/Qualifiers
Domain 60..80
/note= "transmembrane domain"
Domain 99..118
/note= "transmembrane domain"
Domain 129..150
/note= "transmembrane domain"
Domain 181..201
/note= "transmembrane domain"

US5807988-A.

15-SEP-1998.

24-FEB-1994; 94US-00201879.

16-APR-1992; 92US-00869933.

16-APR-1993; 93WO-US003419.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

Jouvin M, Kinet J;

WPI; 1998-520207/44.

N-PSDB; AAV54661.

Human IgE receptor beta subunit protein - and corresponding peptide(s) and fusion protein.

Claim 2; Col 43-44; 55pp; English.

CC This represents the polypeptide sequence of a human beta subunit of Fc
 CC epsilon RI (high-affinity immunoglobulin E receptor). The invention
 CC provides a peptide fragment (AAW75917) from the human Fc epsilon RI beta
 CC subunit protein that contains the amino acid sequence of an ARAM [antigen
 CC recognition activation motif]. Aspects of the invention are methods and
 CC compositions to inhibit the function of human beta subunit, thereby
 CC treating or preventing allergic reactions
 XX
 SQ Sequence 244 AA;

Query Match 100.0%; Score 1238; DB 2; Length 244;
 Best Local Similarity 100.0%; Pred. No. 1.2e-133;
 Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDTESNRANLALPOEPSSVPAFEVLEISPOEVSSGRLLKSSAPPLHTLTLVTKKEQEF 60
 DB 1 MDTESNRANLALPOEPSSVPAFEVLEISPOEVSSGRLLKSSAPPLHTLTLVTKKEQEF 60
 QY 61 LGVTQILTAMICLFCGTVCVSLDISHIEGDIFFSFKAGYPPFWGAIFFSISGMLSIISER 120
 DB 61 LGVTQILTAMICLFCGTVCVSLDISHIEGDIFFSFKAGYPPFWGAIFFSISGMLSIISER 120
 QY 121 RNATYLVRSGLGANTASSIAGGTGTTILINLKSLAYIIHSCQFFETKCFMASFSTE 180
 DB 121 RNATYLVRSGLGANTASSIAGGTGTTILINLKSLAYIIHSCQFFETKCFMASFSTE 180
 QY 181 IVVWMLFLTLGLGSAVSLTICGAGEELKGNKVPEDRVVEELNIYSATYSELEDPCGEMSP 240
 DB 181 IVVWMLFLTLGLGSAVSLTICGAGEELKGNKVPEDRVVEELNIYSATYSELEDPCGEMSP 240
 QY 241 PIDL 244
 DB 241 PIDL 244

RESULT 2
 AAB72900
 ID AAB72900 standard; protein; 244 AA.
 XX
 AC AAB72900;
 DT 15-MAY-2001 (first entry)
 XX
 DE Human IGERB SEQ ID NO: 3.
 XX
 KW Human; immunoglobulin E receptor beta chain; IGERB; chromosome 11q13;
 KW allergy; asthma; rhinitis; eczema; single nucleotide polymorphism; SNP;
 KW atopy; probe; PCR primer.
 XX
 OS Homo sapiens.
 XX
 PN WO200114588-A1.
 XX
 PD 01-MAR-2001.
 XX
 PF 11-AUG-2000; 2000WO-US022175.
 XX
 PR 24-AUG-1999; 99US-0150423P.
 XX
 XX (GENA-) GENAISANCE PHARM INC.
 PA (NAND/) NANDABALAN K.
 XX
 PI Denton RR, Klem SE, Stephens JC;
 XX
 DR WPI; 2001-226623/23.
 DR N-PSDB; AAF92145.
 XX
 PT Novel polynucleotide useful for therapeutic purposes, comprises
 PT nucleotide polymorphisms in immunoglobulin E receptor beta chain gene.
 XX
 XX Claim 10; Page '59-60; 89pp; English.
 PS
 CC The present invention provides the protein and coding sequences of

CC several polymorphic variants of the human immunoglobulin E receptor beta
 CC chain (IGERB). These contain single nucleotide polymorphisms (SNPs) which
 CC may be indicative of a predisposition to atopy, allergy, asthma, rhinitis
 CC and eczema. Also provided are the sequences of probes and primers for use
 CC in identifying the genotype of an individual with regards to the IGERB
 CC gene. The IGERB gene is found at human chromosome 11q13. The sequences
 CC are all useful in therapeutics. The present sequence is the IGERB protein
 XX
 SQ Sequence 244 AA;

Query Match 100.0%; Score 1238; DB 4; Length 244;
 Best Local Similarity 100.0%; Pred. No. 1.2e-133;
 Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDTESNRANLALPOEPSSVPAFEVLEISPOEVSSGRLLKSSAPPLHTLTLVTKKEQEF 60
 DB 1 MDTESNRANLALPOEPSSVPAFEVLEISPOEVSSGRLLKSSAPPLHTLTLVTKKEQEF 60
 QY 61 LGVTQILTAMICLFCGTVCVSLDISHIEGDIFFSFKAGYPPFWGAIFFSISGMLSIISER 120
 DB 61 LGVTQILTAMICLFCGTVCVSLDISHIEGDIFFSFKAGYPPFWGAIFFSISGMLSIISER 120
 QY 121 RNATYLVRSGLGANTASSIAGGTGTTILINLKSLAYIIHSCQFFETKCFMASFSTE 180
 DB 121 RNATYLVRSGLGANTASSIAGGTGTTILINLKSLAYIIHSCQFFETKCFMASFSTE 180
 QY 181 IVVWMLFLTLGLGSAVSLTICGAGEELKGNKVPEDRVVEELNIYSATYSELEDPCGEMSP 240
 DB 181 IVVWMLFLTLGLGSAVSLTICGAGEELKGNKVPEDRVVEELNIYSATYSELEDPCGEMSP 240
 QY 241 PIDL 244
 DB 241 PIDL 244

RESULT 3
 AAB74447
 ID AAB74447 standard; protein; 244 AA.
 XX
 AC AAB74447;
 DT 29-MAY-2001 (first entry)
 XX
 DE Human wild-type Fc epsilon RI beta chain.
 XX
 KW Human; Fc epsilon RI beta chain; immunoglobulin E; allergy; atopy;
 KW conjunctivitis; rhinitis; anaphylaxis; urticaria; angioedema.
 XX
 OS Homo sapiens.
 XX
 PN WO200121816-A1.
 XX
 PD 29-MAR-2001.
 XX
 PF 21-SEP-2000; 2000WO-US025877.
 XX
 PR 21-SEP-1999; 99US-0154924P.
 XX
 XX (ISIS-) ISIS INNOVATION LTD.
 PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 XX
 PI Kinet J, Donnadieu E, Jouvin M, Cookson W, Moffatt MF;
 XX
 DR WPI; 2001-266077/27.
 DR N-PSDB; AAF77688.
 XX
 PT Inhibiting expression of high affinity receptors for immunoglobulin (Ig)
 PT E, in cell or in subject to treat atopy, anaphylaxis mediated by IgE, by
 PT contacting cell or administering to subject, a Fc epsilon chain variant.
 XX
 PS Disclosure; Page 48-49; 55pp; English.
 CC The present invention describes a method of inhibiting the expression of

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OM protein - protein search; using sw model

Run on: March 2, 2006, 18:45:16 ; Search time 27.2346 Seconds
(without alignments)
862.024 Million cell updates/sec

Title: US-10-088-703A-2

Perfect score: 1238

Sequence: 1 MDTESNRRANLALPQEPSSV.....YSATYSELEDPGEMSPIDL 244

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1238	100.0	244	2	A42806
2	766	61.9	152	2	JH0751
3	697.5	56.3	235	2	B34342
4	645.5	52.1	243	2	A31331
5	185.5	15.0	214	2	I59258
6	127	10.3	297	1	A30586
7	123.5	10.0	200	2	JC7585
8	111	9.0	826	2	B55363
9	111	9.0	896	2	A55363
10	103.5	8.4	291	2	A30558
11	96.5	7.8	921	2	E86764
12	94	7.6	466	2	H81697
13	90	7.3	629	2	T22848
14	89	7.2	904	1	RDNTNT
15	86.5	7.0	701	2	F70155
16	86	6.9	722	2	G83685
17	85.5	6.9	377	2	G71341
18	85	6.9	492	2	G75389
19	84.5	6.8	207	2	AF1680
20	84.5	6.8	318	2	H71561
21	84.5	6.8	659	2	E86313
22	84	6.8	681	2	S27868
23	83.5	6.7	380	2	D84214
24	83.5	6.7	470	2	T27326
25	83.5	6.7	473	2	S59365
26	83.5	6.7	669	2	T08827
27	83.5	6.7	4447	2	A69679
28	83	6.7	253	2	T32339
29	83	6.7	440	2	F97098

ALIGNMENTS

RESULT 1

A42806

IgE Fc receptor beta chain - human

C/Species: Homo sapiens (man)

C/Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 09-Jul-2004

C/Accession: A42806; S21154

R/Kuester, H.; Zhang, L.; Brini, A.T.; MacGlashan, D.W.J.; Kinet, J.P.

J. Biol. Chem. 267, 12782-12787, 1992

A/Title: The gene and cDNA for the human high affinity immunoglobulin E receptor beta

A/Reference number: A42806; MUID:92316966; PMID:1535625

A/Accession: A42806

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-244 <KUE>

A/Cross-references: UNIPROT:Q01362; UNIPARC:UPI0000038E6F; GB:M89796; NID:g337417; PII

R/Makawa, K.; Inagawa, N.; Tanaka, Y.; Harada, S.

FEBS Lett. 302, 161-165, 1992

A/Title: Determination of the sequence coding for the beta subunit of the human high-

A/Reference number: S21154; MUID:92339505; PMID:1386024

A/Accession: S21154

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-244 <NAE>

A/Cross-references: UNIPARC:UPI0000038E6F; GB:D10583; NID:g219881; PIDN:BAA01440.1; P:

C/Genetics:

A/Introns: 19/2; 62/3; 107/3; 126/3; 179/3; 212/3

C/Keywords: immunoglobulin receptor; transmembrane protein

Query Match 100.0%; Score 1238; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. No. 3.7e-107;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MDTESNRRANLALPQEPSSVPAFEVLEISPOEVSSGRLLKKSASSPPLHTLTLVKKQE	60
DB	1	MDTESNRRANLALPQEPSSVPAFEVLEISPOEVSSGRLLKKSASSPPLHTLTLVKKQE	60
QY	61	LGVTQLLTAMICLCFGTVCSVLDSHIEDGFSSPKAGYPFWGAIFFSISGMLSI	120
DB	61	LGVTQLLTAMICLCFGTVCSVLDSHIEDGFSSPKAGYPFWGAIFFSISGMLSI	120
QY	121	RNATYLVRSLGANTASSIAGGTGITILLINLKKSLAYIHHSCKQFFETKCFMAGFS	180
DB	121	RNATYLVRSLGANTASSIAGGTGITILLINLKKSLAYIHHSCKQFFETKCFMAGFS	180
QY	181	IIVMMLFLTLGLGSAVSLTICGAEELKGNKVPDRVVEELNIYSATYSELEDPGEM	240
DB	181	IIVMMLFLTLGLGSAVSLTICGAEELKGNKVPDRVVEELNIYSATYSELEDPGEM	240
QY	241	PIDL 244	
DB	241	PIDL 244	

RESULT 2

JH0751
Ige receptor beta chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: JH0751
R:Bieber, T.; de la Salle, H.; Wollenberg, A.; Hakimi, J.; Chizzonite, R.; Ring, J.; Han
J. Exp. Med. 175, 1285-1290, 1992
A:Title: Human epidermal Langerhans cells express the high affinity receptor for immunoglobulin E
A:Reference number: JH0751; MUID:92235608; PMID:1533242
A:Accession: JH0751
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-152 <BIE>
A:Cross-references: UNIPROT:Q14298; UNIPARC:UPI0000073ACE; GB:X66187; NID:G396463; PIDN:

Query Match 61.9%; Score 766; DB 2; Length 152;
Best Local Similarity 98.0%; Pred. No. 1.2e-63;
Matches 149; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 71 ICICFGTWCVSVDISHIEGDFSSFKAGYFPGWGAIFPSISGMLSIISERNATYLVRS 130

Db 1 ICICFGTWCVSVDISHIEGDFSSFKAGYFPGWGAIFPSISGMLSIISERNATYLVRS 60

QY 131 LGANTASSIAGGTGTTILINLKKSLAYIIHSCQKFFETKCFWASPFSTEIVVMMLFTI 190

Db 61 LGANTASSIAGGTGTTILINLKKSLAYIIHSCQKFFETKCFWASPFSTEIVVMMLFTI 120

QY 191 LGLSAVSLTICGAGEELKGNKVPEDRVYBEL 222

Db 121 LGLSAVSLTICGAGEELKGNKVPEDRVYBEL 152

RESULT 3

B34342
Ige Fc receptor beta chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 09-Jul-2004
C:Accession: B34342
R:Ra, C.; Jouvin, M.H.E.; Kinet, J.P.
J. Biol. Chem. 264, 15323-15327, 1989
A:Title: Complete structure of the mouse mast cell receptor for Ige (Fc-epsilon-R1) and
A:Reference number: A34342; MUID:89359361; PMID:2527850
A:Accession: B34342
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-235 <RAC>
A:Cross-references: UNIPROT:P20490; UNIPARC:UPI00000223FC; GB:J05019; NID:g193238; PIDN:
C:Keywords: immunoglobulin receptor; transmembrane protein

Query Match 56.3%; Score 697.5; DB 2; Length 235;
Best Local Similarity 57.7%; Pred. No. 4.4e-57;
Matches 142; Conservative 33; Mismatches 56; Indels 15; Gaps 4;

QY 1 MDTESNRRANLAL--PQEPSSVPAFEVLISPOEVSSGRLLKSASSPPLHTLTLVLKKEQ 58

Db 1 MDTENSRADLALPNQESSAPDIELLEASP-----AKAAPKQTWRTFLKKEQ 50

QY 59 EFLGVTOILTAMICLCFGTWCVSVDISHIEGDFSSFKAGYFPGWGAIFPSISGMLSIIS 118

Db 51 EFLGATQILVGLICLCFGTWCVSVDIEVLLYKLGYPFWGAVLVLSGFLSIIS 110

QY 119 ERNATYLVRSIGANTASSIAGGTGTTILINLKKSLAYIIHSCQKFFETK-CFWASF 177

Db 111 ERKNTLYVRSGANIVSSIAAGTGIALMLILTNWFAY--MNNCKNTEDDGCFCVAF 168

QY 178 STEIVVMMLFLTILGLGSVSLTICGAGEELKGNKVPEDRVYVEELNIYSATYSELEDPCGE 237

Db 169 TTELVLMLFLTILAFCSAVLIIYRIGQELSKVPPDRRLYEELNIYSATYSELEDKGE 228

QY 238 MSPPID 243

Db 229 TSSPVD 234

RESULT 4

A31231
high-affinity Ige receptor beta chain - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C:Accession: A31231
R:Kinet, J.P.; Blank, U.; Ra, C.; White, K.; Metzger, H.; Kochan, J.
Proc. Natl. Acad. Sci. U.S.A. 85, 6483-6487, 1988
A:Title: Isolation and characterization of cDNAs coding for the beta-subunit of the high-affinity
A:Reference number: A31231; MUID:88320465; PMID:2970642
A:Accession: A31231
A:Molecule type: mRNA
A:Residues: 1-243 <KIN>
A:Cross-references: UNIPROT:P13386; UNIPARC:UPI000003FF8D; GB:M22923; GB:J03845; NID:
C:Keywords: immunoglobulin receptor; transmembrane protein

Query Match 52.1%; Score 645.5; DB 2; Length 243;
Best Local Similarity 55.1%; Pred. No. 3e-52;
Matches 135; Conservative 33; Mismatches 70; Indels 7; Gaps 4;

QY 1 MDTESNRRANLAL--PQEPSSVPAFEVLISPOEVSSGRLLKSASSPPLHTLTLVLKKEQ 58

Db 1 MDTENSRADLALPNQESSAPDIELLEASPPAKALPE--KPASPPQQTWQSFLLKEL 58

QY 59 EFLGVTOILTAMICLCFGTWCVSVDISHIEGDFSSFKAGYFPGWGAIFPSISGMLSIIS 118

Db 59 EFLGVTOILVGLICLCFGTWCVSVDIEVLLYKLGYPFWGAVLVLSGFLSIIS 118

QY 119 ERNATYLVRSIGANTASSIAGGTGTTILINLKKSLAYIIHSCQKFFETK-CFWASF 177

Db 119 ERKNTLYVRSGANIVSSIAAGTGIALMLILNLSNAYMNY--CKDITDDGCFVTSP 176

QY 178 STEIVVMMLFLTILGLGSVSLTICGAGEELKGNKVPEDRVYVEELNIYSATYSELEDPCGE 237

Db 177 TTELVLMLFLTILAFCSAVLIIYRIGQELSKVPPDRRLYEELNIYSATYSELEDTRE 236

QY 238 MSPPI 242

Db 237 ASAPV 241

RESULT 5

Ige receptor beta chain / CD20 antigen homolog - human
C:Species: Homo sapiens (man)
C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 05-Nov-1999
C:Accession: I59258
R:Adra, C.N.; Lelias, J.M.; Kobayashi, H.; Kaghad, M.; Morrison, P.; Rowley, J.D.; Lin
Proc. Natl. Acad. Sci. U.S.A. 91, 10178-10182, 1994
A:Title: Cloning of the cDNA for a hematopoietic cell-specific protein related to CD20
A:Reference number: I59258; MUID:95024008; PMID:7524084
A:Accession: I59258
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-214 <RES>
A:Cross-references: UNIPARC:UPI000002EF35; GB:L35848; NID:G561638; PIDN:AAA62319.1; P
C:Keywords: immunoglobulin receptor

Query Match 15.0%; Score 185.5; DB 2; Length 214;
Best Local Similarity 28.5%; Pred. No. 1.1e-09;
Matches 55; Conservative 33; Mismatches 86; Indels 19; Gaps 6;

QY 27 EISPOEVSSGRLLKSASSPPLHTLTLVLKKEQEFILGVTOILTAMICLCFGTWCVSVDIS 86

Db 23 ETGPELNTSVVHPINGSPDQV-----KAKQLVLGAQILNAAMILALGVFLGSLQYPY 76

GenCode version 5.1.7
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OM protein - protein search, using sw model

Run on: March 2, 2006, 18:44:51 ; Search time 180.082 Seconds
(without alignments)
955.947 Million cell updates/sec.

Title: US-10-088-703A-2
Perfect score: 1238
Sequence: 1 MDTESNRRANLALPOEPSSV.....YSATYSELDPGEMSPPIDL 244

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5 .

Searched: 2166443 seqs, 70528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 05.80:.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1238	100.0	244	1 FCERB_HUMAN	Q01362 homo sapien
2	1238	100.0	244	2 Q54A81_HUMAN	Q54A81 homo sapien
3	766	61.9	152	2 Q14298_HUMAN	Q14298 homo sapien
4	697.5	56.3	235	1 FCERB_MOUSE	P20490 mus musculus
5	660.5	53.4	243	2 Q8MJ38_PIG	Q8MJ38 sus scrofa
6	645.5	52.1	243	1 FCERB_RAT	P13386 rattus norv
7	209	16.9	244	1 M4A6B_MOUSE	Q99N09 mus musculus
8	205	16.6	247	2 Q5X1J0_RAT	Q5X1J0 rattus norv
9	201.5	16.3	247	1 M4A6D_MOUSE	Q99N07 mus musculus
10	136	15.8	287	1 M4A8A_MOUSE	Q99N10 mus musculus
11	130	15.3	239	1 M4A4A_HUMAN	Q96J95 homo sapien
12	189.5	15.3	267	1 M4A12_HUMAN	Q99XJ0 homo sapien
13	186.5	15.1	213	1 MS4A3_HUMAN	Q96H15 homo sapien
14	185.5	15.0	214	1 MS4A3_MOUSE	Q920C4 mus musculus
15	185.5	15.0	213	2 Q810H7_MOUSE	Q810H7 mus musculus
16	185.5	15.0	213	2 Q532U3_MOUSE	Q532U3 mus musculus
17	183	14.8	220	2 Q4JF27_HUMAN	Q4JF27 homo sapien
18	182	14.7	679	2 Q96J4A_HUMAN	Q96J4A homo sapien
19	176.5	14.3	217	1 M4A6C_MOUSE	Q99N08 mus musculus
20	174	14.1	250	1 M4A8B_HUMAN	Q9BY19 homo sapien
21	166	13.4	222	2 Q58DM5_BOVIN	Q58DM5 bos taurus
22	165	13.3	240	1 MS4A7_HUMAN	Q99W88 homo sapien
23	165	13.3	240	2 Q6TAG8_HUMAN	Q6TAG8 homo sapien
24	161.5	13.0	241	2 Q567K1_BRARE	Q567K1 brachydanio
25	161	13.0	55	2 Q924W0_MUSSP	Q924W0 mus spretus
26	161	13.0	55	2 P97890_MUSMM	P97890 mus musculus
27	161	13.0	234	2 Q99N04_MOUSE	Q99N04 mus musculus
28	158	12.8	267	2 Q8BV59_MOUSE	Q8BV59 mus musculus
29	157	12.7	234	2 Q8R3W1_MOUSE	Q8R3W1 mus musculus
30	154.5	12.5	197	2 Q810P8_MOUSE	Q810P8 mus musculus
31	152	12.3	248	1 M4A6A_HUMAN	Q9H2W1 homo sapien

RESULT 1	FCERB_HUMAN	STANDARD;	PRT;	244 AA.
ID	FCERB_HUMAN			
AC	Q01362;			
DT	01-APR-1993 (Rel. 25, Created)			
DT	01-APR-1993 (Rel. 25, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	High affinity immunoglobulin epsilon receptor beta-subunit (FCERI)			
DE	(I9E FC receptor, beta-subunit) (Fc epsilon receptor I beta-chain).			
GN	Name=MS4A2; Synonyms=FCER1B, IGER;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=92316966; PubMed=1535625;			
RA	Kuester H., Zhang L., Brini A.T., Macglashan D.W., Kinet J.-P.;			
RT	"The gene and cDNA for the human high affinity immunoglobulin E			
RT	receptor beta chain and expression of the complete human receptor."			
RL	J. Biol. Chem. 267:12782-12787(1992).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=92339505; PubMed=1386024; DOI=10.1016/0014-5793(92)80430-O;			
RA	Maekawa K., Inagawa N., Tanaka Y., Harada S.;			
RT	"Determination of the sequence coding for the beta subunit of the			
RT	human high-affinity I9E receptor."			
RL	FEBS Lett. 302:161-165(1992).			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].			
RC	TISSUE=Lung;			
RX	MEDLINE=23388957; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettman M., Madañ A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madañ A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,			
RA	Schneerch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[4]			

Q8B129	mus musculus
Q5R1M8	felis silve
Q9D3F6	mus musculus
Q80WF0	rattus norv
Q5BLB6	brachydanio
Q567H8	brachydanio
Q99N05	mus musculus
Q4TAI3	tetraodon n
Q8NSU1	homo sapien
P11836	homo sapien
Q5M796	xenopus tro
Q661D5	brachydanio
Q9ES61	mus musculus
Q9H3V2	homo sapien

ALIGNMENTS

RP VARIANT GLY-237.
RX MEDLINE=96414302; PubMed=8817330; DOI=10.1093/hmg/5.7.959;
RA Hill M.R., Cooke W.O.;
RT "A new variant of the beta subunit of the high-affinity receptor for
RT immunoglobulin E (Fc epsilon RI-beta E237G): associations with
RL measures of atopy and bronchial hyper-responsiveness.";
RN Hum. Mol. Genet. 5:959-962(1996).
[5]
RP VARIANT GLY-237.
RX MEDLINE=96440420; PubMed=8842731; DOI=10.1093/hmg/5.8.1129;
RA Shirakawa T., Mao X.-Q., Sasaki S., Enomoto T., Kawai M., Morimoto K.,
RA Hopkin J.;
RT "Association between atopic asthma and a coding variant of Fc-epsilon-
RT RI-beta in a Japanese population.";
RL Hum. Mol. Genet. 5:1129-1130(1996).
[6]
RN ERRATUM.
RP MEDLINE=97123518; PubMed=8968765;
RA Shirakawa T., Mao X.-Q., Sasaki S., Enomoto T., Kawai M., Morimoto K.,
RA Hopkin J.;
RL Hum. Mol. Genet. 5:2068-2068(1996).
CC -1- FUNCTION: Binds to the Fc region of immunoglobulins epsilon. High
CC affinity receptor. Responsible for initiating the allergic
CC response. Binding of allergen to receptor-bound IgE leads to cell
CC activation and the release of mediators (such as histamine)
CC responsible for the manifestations of allergy. The same receptor
CC also induces the secretion of important lymphokines.
CC -1- SUBUNIT: Tetramer of an alpha chain, a beta chain, and two
CC disulfide linked gamma chains.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Found on the surface of mast cells and
CC basophils.
CC -1- POLYMORPHISM: Variant Glu-237 has been found to be present in
CC about 5.3% of a 1004 individuals population sample in Australia.
CC It seems to be a risk factor for atopic dermatitis and asthma.
CC -1- SIMILARITY: Belongs to the MS4A family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC ENBL; D10583; BAA01440.1; -; mRNA.
CC DR ENBL; M89796; AAA60269.1; -; Genomic DNA.
CC DR ENBL; BC074800; AAH74800.1; -; mRNA.
CC DR ENBL; BC074843; AAH74843.1; -; mRNA.
CC DR PIR; A42806; A42806.
CC DR Ensembl; ENSG00000149534; Homo sapiens.
CC HGNC; HGNC:7316; MS4A2.
CC DR MTM; 147138; -.
CC DR GO; GO:0005887; C: integral to plasma membrane; TAS.
CC DR GO; GO:0005262; F: calcium channel activity; TAS.
CC DR GO; GO:0008283; P: cell proliferation; TAS.
CC DR GO; GO:0007186; P: G-protein coupled receptor protein signaling. . . ; TAS.
CC DR GO; GO:0006959; P: humoral immune response; TAS.
CC DR InterPro; IPR007237; CD20/IgEFCrecept.
CC DR Pfam; PF04103; CD20; 1.
CC DR ICG-binding protein; Multigene family; Polymorphism; Receptor;
KW Transmembrane. 1 59 Cytoplasmic (Potential).
FT TOPO_DOM 60 79 Potential.
FT TRANSMEM 80 97 Extracellular (Potential).
FT TOPO_DOM 98 117 Potential.
FT TRANSMEM 118 130 Cytoplasmic (Potential).
FT TOPO_DOM 131 150 Potential.
FT TRANSMEM 151 180 Extracellular (Potential).
FT TOPO_DOM 181 200 Potential.
FT TRANSMEM 201 244 Cytoplasmic (Potential).
FT TOPO_DOM 237 237 E -> G (in dbSNP:569108).
FT VARIANT 237 237 /FTid=VAR_003965.
SQ SEQUENCE 244 AA; 26534 MW; CE523102D5F567AF CRC64;

Query Match 100.0%; Score 1238; DB 1; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.3e-105;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MOTESNRRANLALPOEPSSVPAFEVLEISPOEVSSGRLLKSASSPPLHTLWTLVTKKEQEF 60
DB 1 MOTESNRRANLALPOEPSSVPAFEVLEISPOEVSSGRLLKSASSPPLHTLWTLVTKKEQEF 60
QY 61 LGVTQILTAMICLCFGTVVCSVLDISHIEGDIFFSPFKAGYPFWGAIFPFSIGMLSIISER 120
DB 61 LGVTQILTAMICLCFGTVVCSVLDISHIEGDIFFSPFKAGYPFWGAIFPFSIGMLSIISER 120
QY 121 RNATYLVRSGLGANTASSIAGGTGTTILINLKSLAYIHHSCKQFFETKCFMASFSTE 180
DB 121 RNATYLVRSGLGANTASSIAGGTGTTILINLKSLAYIHHSCKQFFETKCFMASFSTE 180
QY 181 IVVMMFLFTILGLGSAVSLTICGAGEELKGNKVPEDRVVYEELNIYSATYSELEDPCGEMSP 240
DB 181 IVVMMFLFTILGLGSAVSLTICGAGEELKGNKVPEDRVVYEELNIYSATYSELEDPCGEMSP 240
QY 241 PIDL 244
DB 241 PIDL 244
RESULT 2
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ID Q54A81_HUMAN PRELIMINARY; PRT; 244 AA.
AC Q54A81;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Fc-epsilon receptor I beta-chain.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=12697656; DOI=10.1093/intimm/dxg055;
RA Akizawa Y., Nishiyama C., Hasegawa M., Maeda K., Nakahata T.,
RA Okumura K., Ra C., Ogawa H.;
RT "Regulation of human Fc epsilon RI beta chain gene expression by Oct-
RT 1.1";
RL Int. Immunol. 15:549-556(2003).
DR EMBL; AB080913; BAC66486.1; -; Genomic DNA.
KW Receptor.
SQ SEQUENCE 244 AA; 26533 MW; CE523102D5F567AF CRC64;
Query Match 100.0%; Score 1238; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.3e-105;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MOTESNRRANLALPOEPSSVPAFEVLEISPOEVSSGRLLKSASSPPLHTLWTLVTKKEQEF 60
DB 1 MOTESNRRANLALPOEPSSVPAFEVLEISPOEVSSGRLLKSASSPPLHTLWTLVTKKEQEF 60
QY 61 LGVTQILTAMICLCFGTVVCSVLDISHIEGDIFFSPFKAGYPFWGAIFPFSIGMLSIISER 120
DB 61 LGVTQILTAMICLCFGTVVCSVLDISHIEGDIFFSPFKAGYPFWGAIFPFSIGMLSIISER 120
QY 121 RNATYLVRSGLGANTASSIAGGTGTTILINLKSLAYIHHSCKQFFETKCFMASFSTE 180
DB 121 RNATYLVRSGLGANTASSIAGGTGTTILINLKSLAYIHHSCKQFFETKCFMASFSTE 180
QY 181 IVVMMFLFTILGLGSAVSLTICGAGEELKGNKVPEDRVVYEELNIYSATYSELEDPCGEMSP 240
DB 181 IVVMMFLFTILGLGSAVSLTICGAGEELKGNKVPEDRVVYEELNIYSATYSELEDPCGEMSP 240
QY 241 PIDL 244
DB 241 PIDL 244

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OM protein - protein search, using sw model

Run on: March 2, 2006, 18:46:52 ; Search time 20.5649 seconds
(without alignments)
980.936 Million cell updates/sec

Title: US-10-088-703A-2
Perfect score: 1238
Sequence: 1 MDTESNRANLALPQPSV.....YSATYSELDPGEMSPIDL 244

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/prodata/1/iaa/5 COMB.pep.*
- 2: /cgn2_6/prodata/1/iaa/6 COMB.pep.*
- 3: /cgn2_6/prodata/1/iaa/H COMB.pep.*
- 4: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep.*
- 5: /cgn2_6/prodata/1/iaa/RE COMB.pep.*
- 6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1238	100.0	244	1	US-07-869-933-32
2	1238	100.0	244	1	US-08-201-879A-3
3	1238	100.0	244	2	US-09-103-663-32
4	1238	100.0	244	2	US-09-949-016-5892
5	1238	100.0	244	2	US-09-949-016-8329
6	697.5	56.3	235	1	US-07-869-933-34
7	697.5	56.3	235	1	US-08-201-879A-5
8	697.5	56.3	235	2	US-09-103-663-34
9	645.5	52.1	243	1	US-07-869-933-29
10	645.5	52.1	243	1	US-07-869-933-33
11	645.5	52.1	243	1	US-08-201-879A-4
12	645.5	52.1	243	1	US-08-916-902A-4
13	645.5	52.1	243	1	US-09-213-389-4
14	645.5	52.1	243	2	US-09-103-663-29
15	645.5	52.1	243	2	US-09-103-663-33
16	645.5	52.1	246	1	US-07-869-933-23
17	645.5	52.1	246	2	US-09-103-663-23
18	200.5	16.2	247	2	US-09-124-864-49
19	190	15.3	239	1	US-08-916-902A-1
20	190	15.3	239	1	US-09-213-389-1
21	190	15.3	239	2	US-10-164-595-74
22	189.5	15.3	239	2	US-09-904-615-73
23	189.5	15.3	239	2	US-10-054-988-73
24	185.5	15.0	214	1	US-08-318-492-4
25	185.5	15.0	214	1	US-08-707-340-4
26	185.5	15.0	214	1	US-08-916-902A-3
27	185.5	15.0	214	1	US-08-994-578-4

28	185.5	15.0	214	1	US-09-213-389-3	Sequence 3, Appli
29	183.5	14.8	307	2	US-09-904-615-142	Sequence 142, App
30	183.5	14.8	307	2	US-10-054-988-142	Sequence 142, App
31	174	14.1	250	2	US-09-702-705-1677	Sequence 1677, Ap
32	174	14.1	250	2	US-09-736-457-1677	Sequence 1677, Ap
33	174	14.1	250	2	US-09-671-325-1677	Sequence 1677, Ap
34	174	14.1	250	2	US-09-658-824-1677	Sequence 1677, Ap
35	174	14.1	250	2	US-10-017-754-1677	Sequence 1677, Ap
36	174	14.1	250	2	US-10-017-754-2004	Sequence 2004, Ap
37	174	14.1	250	2	US-09-651-563-1677	Sequence 1677, Ap
38	166	13.4	250	2	US-10-017-754-1874	Sequence 1874, Ap
39	166	13.4	286	2	US-10-017-754-1878	Sequence 1878, Ap
40	166	13.4	384	2	US-10-017-754-1876	Sequence 1876, Ap
41	152	12.3	248	2	US-09-489-847-207	Sequence 207, App
42	152	12.3	273	2	US-09-489-847-363	Sequence 363, App
43	144	11.6	204	2	US-09-904-615-117	Sequence 117, App
44	144	11.6	204	2	US-10-054-988-117	Sequence 117, App
45	142.5	11.5	225	2	US-09-855-323-14	Sequence 14, Appli

ALIGNMENTS

RESULT 1
US-07-869-933-32
; Sequence 32, Application US/07869933
; Patent No. 5770396
; GENERAL INFORMATION:
; APPLICANT: KINET, Jean-Pierre
; TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
; TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/869,933
; FILING DATE: 19920416
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 40399/154 NIHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO.: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 244 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; STRAIN: FcR1 beta subunit
; US-07-869-933-32

Query Match 100.0%; Score 1238; DB 1; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.2e-132;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDTESNRANLALPQPSVPAPEVLEISPVQVSSGRLLKSASSPPLHTLTLVTKKEQEF 60

Db 1 MDTESNRANLALPOEPSSVPAFEVLEISPOEVSSGRLLKSASSPPLHTWLTVLKKEQEF 60
QY 61 LGVTQILTAMICLCFGTVCVSLDISHIEGDIFFSSFKAGYPPFWGAIFFSISGMLSIISER 120
Db 61 LGVTQILTAMICLCFGTVCVSLDISHIEGDIFFSSFKAGYPPFWGAIFFSISGMLSIISER 120
QY 121 RNATYLVRSGLGANTASSIAGGTGTTILINLKSLAYIHHSCKQFFETKCFMASPSTE 180
Db 121 RNATYLVRSGLGANTASSIAGGTGTTILINLKSLAYIHHSCKQFFETKCFMASPSTE 180
QY 181 IVVMMLFTILGLGSAVSLTICGAGEELKGNKVPEDRVYVEELNIYSATYSELEDPCGEMSP 240
Db 181 IVVMMLFTILGLGSAVSLTICGAGEELKGNKVPEDRVYVEELNIYSATYSELEDPCGEMSP 240
QY 241 PIDL 244
Db 241 PIDL 244

RESULT 2

US-08-201-879A-3
; Sequence 3, Application US/08201879A
; Patent No. 5807988
; GENERAL INFORMATION:
; APPLICANT: KINET, Jean-Pierre
; TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
; TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
; TITLE OF INVENTION: IMMUNOGLOBULIN E
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/201,879A
; FILING DATE: 24-FEB-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/869,933
; FILING DATE: 16-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/03419
; FILING DATE: 16-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 40399/234/NIHD
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELETYPE: 904136
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 244 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-201-879A-3

Query Match 100.0%; Score 1238; DB 1; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.2e-132;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDTESNRANLALPOEPSSVPAFEVLEISPOEVSSGRLLKSASSPPLHTWLTVLKKEQEF 60
Db 1 MDTESNRANLALPOEPSSVPAFEVLEISPOEVSSGRLLKSASSPPLHTWLTVLKKEQEF 60
QY 61 LGVTQILTAMICLCFGTVCVSLDISHIEGDIFFSSFKAGYPPFWGAIFFSISGMLSIISER 120
Db 61 LGVTQILTAMICLCFGTVCVSLDISHIEGDIFFSSFKAGYPPFWGAIFFSISGMLSIISER 120
QY 121 RNATYLVRSGLGANTASSIAGGTGTTILINLKSLAYIHHSCKQFFETKCFMASPSTE 180
Db 121 RNATYLVRSGLGANTASSIAGGTGTTILINLKSLAYIHHSCKQFFETKCFMASPSTE 180
QY 181 IVVMMLFTILGLGSAVSLTICGAGEELKGNKVPEDRVYVEELNIYSATYSELEDPCGEMSP 240
Db 181 IVVMMLFTILGLGSAVSLTICGAGEELKGNKVPEDRVYVEELNIYSATYSELEDPCGEMSP 240
QY 241 PIDL 244
Db 241 PIDL 244

RESULT 3

US-09-103-663-32
; Sequence 32, Application US/09103663D
; Patent No. 6171803
; GENERAL INFORMATION:
; APPLICANT: Kinet et al.
; TITLE OF INVENTION: Isolation, characterization, and use of the human beta
; TITLE OF INVENTION: subunit of the high affinity receptor for
; TITLE OF INVENTION: immunoglobulin E.
; FILE REFERENCE: 50490
; CURRENT APPLICATION NUMBER: US/09/103,663D
; CURRENT FILING DATE: 1998-06-23
; EARLIER APPLICATION NUMBER: 07/869,933
; EARLIER FILING DATE: 1992-04-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-103-663-32

Query Match 100.0%; Score 1238; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.2e-132;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDTESNRANLALPOEPSSVPAFEVLEISPOEVSSGRLLKSASSPPLHTWLTVLKKEQEF 60
Db 1 MDTESNRANLALPOEPSSVPAFEVLEISPOEVSSGRLLKSASSPPLHTWLTVLKKEQEF 60
QY 61 LGVTQILTAMICLCFGTVCVSLDISHIEGDIFFSSFKAGYPPFWGAIFFSISGMLSIISER 120
Db 61 LGVTQILTAMICLCFGTVCVSLDISHIEGDIFFSSFKAGYPPFWGAIFFSISGMLSIISER 120
QY 121 RNATYLVRSGLGANTASSIAGGTGTTILINLKSLAYIHHSCKQFFETKCFMASPSTE 180
Db 121 RNATYLVRSGLGANTASSIAGGTGTTILINLKSLAYIHHSCKQFFETKCFMASPSTE 180
QY 181 IVVMMLFTILGLGSAVSLTICGAGEELKGNKVPEDRVYVEELNIYSATYSELEDPCGEMSP 240
Db 181 IVVMMLFTILGLGSAVSLTICGAGEELKGNKVPEDRVYVEELNIYSATYSELEDPCGEMSP 240
QY 241 PIDL 244
Db 241 PIDL 244

RESULT 4

US-09-949-016-5892
; Sequence 5892, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 2, 2006, 18:50:58 ; Search time 67.8087 Seconds
(without alignments)
1503.501 Million cell updates/sec

Title: US-10-088-703A-2
Perfect score: 1238
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing: first 45 summaries

Database : Published Applications AA Main:
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1238	100.0	244	US-10-369-214-124	Sequence 124, App
2	1238	100.0	244	US-10-433-287-42	Sequence 42, Appl
3	697.5	56.3	235	US-10-369-214-123	Sequence 123, App
4	697.5	56.3	235	US-10-433-287-50	Sequence 50, Appl
5	645.5	52.1	243	US-10-433-287-52	Sequence 52, Appl
6	209	16.9	244	US-10-433-287-28	Sequence 28, Appl
7	201.5	16.3	247	US-10-433-287-32	Sequence 32, Appl
8	200.5	16.2	247	US-09-866-050A-687	Sequence 687, App
9	196	15.8	268	US-10-433-287-36	Sequence 36, Appl
10	191	15.4	197	US-10-295-027-452	Sequence 452, App
11	191	15.4	220	US-10-015-115-103	Sequence 103, App
12	191	15.4	239	US-10-015-115-101	Sequence 101, App
13	190	15.3	220	US-10-295-027-1310	Sequence 1310, App
14	190	15.3	220	US-10-264-237-2693	Sequence 2693, App
15	190	15.3	220	US-10-433-287-2	Sequence 2, Appli
16	190	15.3	239	US-10-015-115-102	Sequence 102, App
17	190	15.3	239	US-10-717-665-74	Sequence 74, Appl
18	190	15.3	245	US-09-374-046A-152	Sequence 152, App
19	190	15.3	245	US-10-616-263-152	Sequence 152, App
20	189.5	15.3	267	US-09-981-353-82	Sequence 82, Appl
21	189.5	15.3	273	US-10-450-763-47363	Sequence 47363, A
22	189.5	15.3	299	US-09-739-254-73	Sequence 73, Appl
23	189.5	15.3	299	US-09-904-615-73	Sequence 73, Appl
24	189.5	15.3	299	US-10-054-988-73	Sequence 73, Appl
25	186.5	15.1	214	US-10-157-031-104	Sequence 104, App
26	186	15.0	267	US-10-433-287-46	Sequence 46, Appl
27	185.5	15.0	214	US-10-433-287-44	Sequence 44, Appl

28	184	14.9	240	5	US-10-484-148-7	Sequence 7, Appli
29	183.5	14.8	307	3	US-09-739-254-142	Sequence 142, App
30	183.5	14.8	307	3	US-09-904-615-142	Sequence 142, App
31	183.5	14.8	307	4	US-10-054-988-142	Sequence 142, App
32	178	14.4	227	5	US-10-450-763-49595	Sequence 49595, A
33	176.5	14.3	217	4	US-10-433-287-30	Sequence 30, Appl
34	174	14.1	250	3	US-09-736-457-1677	Sequence 1677, Ap
35	174	14.1	250	3	US-09-902-941-1677	Sequence 1677, Ap
36	174	14.1	250	3	US-09-849-626-1677	Sequence 1677, Ap
37	174	14.1	250	4	US-10-017-754-1677	Sequence 1677, Ap
38	174	14.1	250	4	US-10-017-754-2004	Sequence 2004, Ap
39	174	14.1	250	4	US-10-156-136-21	Sequence 21, Appl
40	174	14.1	250	4	US-10-113-872-1677	Sequence 1677, Ap
41	174	14.1	250	4	US-10-113-872-2004	Sequence 2004, Ap
42	174	14.1	250	4	US-10-283-017-1677	Sequence 1677, Ap
43	174	14.1	250	4	US-10-283-017-2004	Sequence 2004, Ap
44	174	14.1	250	4	US-10-295-027-624	Sequence 624, App
45	174	14.1	250	4	US-10-264-237-2566	Sequence 2566, Ap

ALIGNMENTS

RESULT 1

US-10-369-214-124
; Sequence 124, Application US/10369214
; Publication No. US20030232037A1
; GENERAL INFORMATION:
; APPLICANT: Groot, Pieter C.
; APPLICANT: Berghenhegouwen van, Bram J.
; APPLICANT: Oosterhout van, Antoon J.M.
; TITLE OF INVENTION: Genes involved in immune related responses observed
; TITLE OF INVENTION: with asthma
; FILE REFERENCE: P53837US00
; CURRENT APPLICATION NUMBER: US/10/369,214
; CURRENT FILING DATE: 2003-02-15
; PRIOR APPLICATION NUMBER: EP 00202867.8
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: PCT/NL01/00610
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 124
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(244)
; OTHER INFORMATION: /note="Ige receptor beta chain"
US-10-369-214-124

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Best Local Similarity	100.0%;	Pred. No. 1.9e-122;		
Matches 244;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MDTESNRANLALPQEPSSVPAFEVLEISPOEVSSGRLLKLSASSPPLHTWLTVLKKEQEF	60	
Db	1	MDTESNRANLALPQEPSSVPAFEVLEISPOEVSSGRLLKLSASSPPLHTWLTVLKKEQEF	60	
QY	61	LGVTQILTAMICLCFCGTVCVSLDISHIEDGIFSSFKAGYPPFWGAIFFSISGMLSIISER	120	
Db	61	LGVTQILTAMICLCFCGTVCVSLDISHIEDGIFSSFKAGYPPFWGAIFFSISGMLSIISER	120	
QY	121	RNATYIVRSGLSANTASSIAGGTGITILLINKKSLAYIIHSCQKFFETKCFMASFSTE	180	
Db	121	RNATYIVRSGLSANTASSIAGGTGITILLINKKSLAYIIHSCQKFFETKCFMASFSTE	180	
QY	181	IYVMMFLFTILGGSVSLTICGAEELKGNKVPDRVVEELNIYSATYSELEDPGEMSP	240	
Db	181	IYVMMFLFTILGGSVSLTICGAEELKGNKVPDRVVEELNIYSATYSELEDPGEMSP	240	
QY	241	PIDL 244		

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 2, 2006, 18:51:46 ; Search time 9.44875 Seconds
(without alignments)
516.474 Million cell updates/sec

Title: US-10-088-703A-2

Perfect score: 1238
Sequence: 1 MDTESNRANLALPQPPSSV.....YSATYSELDPGEMSPIDL 244

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 135339 seqs, 20000136 residues

Total number of hits satisfying chosen parameters: 135339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep.*
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5: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pep.*
6: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	186	15.0	267	US-10-506-443A-38	Sequence 38, Appl
2	147.5	11.9	298	US-11-138-949-9	Sequence 9, Appl
3	143.5	11.6	297	US-11-138-949-6	Sequence 6, Appl
4	128	10.3	248	US-09-378-360A-610	Sequence 610, Appl
5	127	10.3	297	US-11-138-949-7	Sequence 7, Appl
6	127	10.3	297	US-11-190-364-25	Sequence 25, Appl
7	127	10.3	297	US-11-190-364-25	Sequence 26, Appl
8	127	10.3	297	US-11-147-780-25	Sequence 25, Appl
9	127	10.3	297	US-11-147-780-26	Sequence 26, Appl
10	123.5	10.0	199	US-11-179-018-2	Sequence 2, Appl
11	111	9.0	896	US-11-080-991-98	Sequence 98, Appl
12	106	8.6	20	US-10-485-788A-598	Sequence 598, Appl
13	103.5	8.4	291	US-11-138-949-8	Sequence 8, Appl
14	100	8.1	138	US-11-179-018-6	Sequence 6, Appl
15	99.5	8.0	149	US-11-179-018-8	Sequence 8, Appl
16	90.5	7.3	391	US-10-793-626-1236	Sequence 1236, Appl
17	83.5	6.7	230	US-11-072-512-3554	Sequence 3554, Appl
18	81.5	6.6	437	US-11-087-099-6210	Sequence 6210, Appl
19	81.5	6.6	452	US-10-793-626-1834	Sequence 1834, Appl
20	80	6.5	478	US-11-072-512-2616	Sequence 2616, Appl
21	79.5	6.4	756	US-10-330-773-731	Sequence 731, Appl
22	79.5	6.4	935	US-10-995-561-1012	Sequence 1012, Appl
23	79.5	6.4	935	US-10-995-561-1013	Sequence 1013, Appl
24	78	6.3	237	US-11-108-172-1062	Sequence 1062, Appl
25	78	6.3	243	US-11-108-172-1122	Sequence 1122, Appl

26	6.3	446	7	US-11-108-172-1121	Sequence 1121, Appl
27	77	394	6	US-10-821-234-1194	Sequence 1194, Appl
28	76.5	972	6	US-10-821-234-1597	Sequence 1597, Appl
29	76	6.1	608	US-11-167-856-12	Sequence 12, Appl
30	74	6.0	172	US-11-036-797-36	Sequence 36, Appl
31	74	6.0	461	US-11-072-512-3584	Sequence 3584, Appl
32	74	6.0	479	US-11-087-099-2079	Sequence 2079, Appl
33	73.5	5.9	359	US-11-087-177-29	Sequence 29, Appl
34	73	344	7	US-11-108-172-1085	Sequence 1085, Appl
35	72.5	5.9	268	US-10-793-626-1830	Sequence 1830, Appl
36	72.5	5.9	365	US-11-087-099-3888	Sequence 3888, Appl
37	72.5	5.9	1228	US-11-234-786-537	Sequence 537, Appl
38	72.5	5.9	1261	US-11-234-786-538	Sequence 538, Appl
39	72.5	5.9	1325	US-10-329-258-10	Sequence 10, Appl
40	72.5	5.9	1325	US-11-124-367A-410	Sequence 410, Appl
41	72.5	5.9	5712	US-11-143-980-47	Sequence 47, Appl
42	72	263	7	US-11-087-099-9836	Sequence 9836, Appl
43	72	5.8	479	US-11-087-099-2356	Sequence 2356, Appl
44	72	5.8	652	US-11-079-122-11	Sequence 11, Appl
45	71.5	5.8	112	US-11-098-686-11412	Sequence 11412, A

ALIGNMENTS

RESULT 1
US-10-506-443A-38
; Sequence 38, Application US/10506443A
; Publication No. US20060013817A1
; GENERAL INFORMATION:
; APPLICANT: Sahin Dr., Ugur
; APPLICANT: Tureci Dr., Ozlem
; APPLICANT: Koslowski Dr., Michael
; TITLE OF INVENTION: Genetic Products Differentially Expressed in Tumors and Use The
; FILE REFERENCE: 342-3PCT
; CURRENT APPLICATION NUMBER: US/10/506,443A
; CURRENT FILING DATE: 2004-09-01
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-506-443A-38

Query Match 15.0%; Score 186; DB 6; Length 267;
Best Local Similarity 30.5%; Pred. No. 2.9e-11;
Matches 47; Conservative 30; Mismatches 59; Indels 18; Gaps 3;
QY 44 SPPLHTLTLVKKQEFGLGVTQILTAMICLCFGTVVCSV-LDISHIEGDIFFSFKAGYPF 102
DB 74 NPSVGTAVNWFEEAKALGVQIMVGLMHIGFVLCISFVSFREVLFSTAVIGYYPF 133
QY 103 WGAIFPSISGMLSIISERRNATYLVRSIGANTASSIAGTGITLIIINL-----152
DB 134 WGGLSFIISGSLVSASKELSRCLVKGLGMINIVSILAFIGVILLVDMCINGVAGODY 193
QY 153 -----KSLAYIHHSCKPFETKCFMASPSTE 180
DB 194 WAVLSGKGISATLMIFSLLEFF-VACATAHFANQ 226
RESULT 2
US-11-138-949-9
; Sequence 9, Application US/11138949
; Publication No. US20050271662A1
; GENERAL INFORMATION:
; APPLICANT: Reall, Melissa J
; TITLE OF INVENTION: CANINE CD20 COMPOSITIONS
; FILE REFERENCE: 04-457A
; CURRENT APPLICATION NUMBER: US/11/138,949
; CURRENT FILING DATE: 2005-05-26
; PRIOR APPLICATION NUMBER: 60/575172

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; PRIOR FILING DATE: 2004-05-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Felis catus
US-11-138-949-9

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Best Local Similarity 22.6%; Pred.No.2.5e-07;
Matches 68; Conservative 48; Mismatches 112; Indels 73; Gaps 12;

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Qy 61 LGVTQLLTAMICLCFGTVVCSVLDSIHIEDIFSSFRAGYPFWGAIFFSISGMLSIISER 120
Db 52 LGAVQIMNGLFHMAIGLL-----MIHMEVYAPICMTVWVPLWGGIMVILISGSLLVAAEK 106
Qy 121 RNATYLVRSLGANTASSIAGCTITLIIN-----LKKSLAYTHHS 163
Db 107 NPKRSLVKGWIMNLSLFAAISGMILLIMDIFNIAISHFFKFMENLLKSPKPYIDIHT 166
Qy 164 CO-----KPFET--KCFMASFSTEIVVMMLFLTILGL-----SA 196
Db 167 QPESKPSEKNLSIKYCDIRSIVLSFAV-MVVFTLFOKLVTAGVIVENWKLCSPK 225
Qy 197 VSLITICAGBELKGN--KVPEDRV-----YEELNIYSATYSELEDPEGMS---PPI 242
Db 226 ADVVVLAAEKEQLVEITEEAVELTEVSSQPKNEEDIIIPVQEEETEEMNFPPEPQ 295
Qy 243 D 243
Db 286 D 286

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RESULT 3
US-11-138-949-6.
; Sequence 6, Application US/11138949
; Publication No. US20050271662A1
; GENERAL INFORMATION:
; APPLICANT: Beall, Melissa J
; TITLE OF INVENTION: CANINE CD20 COMPOSITIONS
; FILE REFERENCE: 04-457A
; CURRENT APPLICATION NUMBER: US/11/138,949
; CURRENT FILING DATE: 2005-05-26
; PRIOR APPLICATION NUMBER: 60/575172
; PRIOR FILING DATE: 2004-05-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.3.
; SEQ ID NO 6
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Canis familiaris
US-11-138-949-6

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Query Match      11.6%; Score 143.5; DB 7; Length 297;
Best Local Similarity 24.3%; Pred. No. 6.3e-07;
Matches         45; Conservative 33; Mismatches 68; Indels 39; Gaps 7;

QY 1 MOTESRRANLALPQEPSSVPA--FEVLEISPOEVSSGRLLKKSASPLHTWLTVLKKEQ 58
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Db 1 MTTPRNSMG-TLPVDPMKSPMTAMPVQKIIPK-----MPSVVGQTQNF--RES 49

QY 59 EFLGVQILTAMTCLFGTVCSVLDSHIEGDIFF--SPKAGYPFWGAIFFISGMLSI 116
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Db 50 KTLGAVQIMNGLFHIALGSLM-----IHTDVYAPICITMYPLWGGIMFIISGSLA 102

QY 117 ISERRNATYLVRLSGLGANTASSIAGTGITILIN-----LKKSLAYI 159
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :
Db 103 AADKPNRKSLVKGKIMNLSLFAA:SGIIFLMDIFNITISHFLKQENLNLIKAPIVY 162

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QY	160	HHSC	164
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Db	163	DIHNC	167

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RESULT 4
US-09-978-360A-610
; Sequence 610, Application US/09978360A
; Publication No. US2006009633A9
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste Dumas Milne
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; APPLICANT: Clusel, Catherine
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: 56.US4.CIP
; CURRENT APPLICATION NUMBER: US/09/978.360A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: US 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: US 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: US 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 60/099,273
; PRIOR FILING DATE: -09-04
; PRIOR APPLICATION NUMBER: US 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: US 09/215,435
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: PCT/IB98/02122
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: US 09/247,155
; PRIOR FILING DATE: 1999-02-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 810
; SOFTWARE: Patent.pm
; SEQ ID NO 610
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -69..-1
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (-25, 65, 79, 83, 90, 91, 94, 106, 112, 130, 131, 155)
; OTHER INFORMATION: unknown
US-09-978-360A-610

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Query Match	10.3%	Score 128;	DB 5;	Length 248;
Best Local Similarity	23.2%;	Pred. No. 1.8e-05;		
Matches	59;	Conservative 35;	Mismatches 102;	Indels 58; Gaps 9;
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QY	68	TAMICLCFTGVVCSVL---DISHIEDGIPSSKAGYPPFWGAIFFSISGMLSIISERNAT	124	
DB	55	CGMVLISGIIILASASFSNFTQVSTLLNS--AYPTGPPFFFIISGSLSIATKKRLTN	111	
QY	125	YLVRGSLGANTASSIAGGTGTIILII-----NLKKSLAYIIHHSQKFF	168	
DB	112	LLVHTTLVGSIIISALSAVGFTXLSVKQATLNPASLXCXLKXNPTXXIVYFYHDSLY	171	
QY	169	ETKCFMA-SFSTEIVVMMLFLTILGI-----GSAVSLTICGAGEEL	208	

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: March 2, 2006, 18:41:26 ; Search time 55.9681 Seconds
(without alignments)
1530.851 Million cell updates/sec

Title: US-10-088-703A-4

Perfect score: 1002

Sequence: 1 MDTESNRRNALPQEPSSV.....SFSTVCIFFCVGRLEFRWFLM 195

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Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1002	100.0	195	4	AAB74448 Human var
2	910	90.8	244	2	AAB74448 Human hig
3	910	90.8	244	2	AAB75918 Human bet
4	910	90.8	244	4	AAB72900 Human IGE
5	910	90.8	244	4	AAB74447 Human wil
6	910	90.8	244	5	ABP65043 Human mem
7	910	90.8	244	5	AAB80021 Human IGE
8	910	90.8	244	8	ADQ90468 Human IGE
9	492	49.1	235	5	ABP65047 Mouse mem
10	492	49.1	235	5	AAB80020 Mouse IGE
11	492	49.1	235	8	ADQ90467 Mouse IGE
12	475	47.4	243	2	AAR42341 Subunit o
13	475	47.4	243	5	ABP65048 Rat membr
14	475	47.4	246	2	AAR14770 Beta subu
15	475	47.4	246	2	AAR42337 Human fce
16	466	46.5	243	2	AAR05026 Beta subu
17	283	28.2	112	2	AAR05027 Deleted f
18	283	28.2	115	2	AAR14771 Truncated
19	189.5	18.9	244	4	AAG63825 Immunogl
20	188.5	18.8	244	5	ABP65036 Mouse mem
21	188.5	18.8	679	5	ADQ82232 Human tes
22	187.5	18.7	267	2	AAY15224 Human rec
23	187.5	18.7	267	6	ADA10964 Human CDN
24	187.5	18.7	273	4	ABG17004 Novel hum

25	187.5	18.7	299	3	AAY91352 Human sec
26	187.5	18.7	308	5	ADR41397 Human CD-
27	186.5	18.6	268	5	ABP65040 Mouse mem
28	184	18.4	267	5	ABP65045 Human mem
29	184	18.4	267	7	ADL13125 Human MS4
30	184	18.4	267	9	ADY91718 Human mem
31	184	18.4	267	9	AEA04513 Human pro
32	183	18.3	247	5	ABP65038 Mouse mem
33	182.5	18.2	240	7	ADC42847 REMAP pro
34	182	18.2	247	4	AAR05353 Mouse hig
35	182	18.2	247	5	ABB72363 Murine pr
36	181.5	18.1	307	3	AAY91421 Human sec
37	178	17.8	197	7	ADN39134 Cancer/an
38	177	17.7	220	5	ABB90317 Human pol
39	177	17.7	220	5	ABP65023 Human mem
40	177	17.7	220	6	ABR55608 Amino aci
41	177	17.7	220	7	ADN39992 Cancer/an
42	177	17.7	220	8	ADP25105 PRO polyp
43	177	17.7	220	8	ADU06669 Novel bro
44	177	17.7	239	2	AAR96745 High affi
45	177	17.7	239	3	AAY50174 Human hig

ALIGNMENTS

RESULT 1
AAB74448
ID AAB74448 standard; protein; 195 AA.
XX
AC AAB74448;
XX
DT 29-MAY-2001 (first entry)
XX
DE Human variant FcpsiIonRibeta chain.
XX
KW Human; FcpsiIonRibeta chain; immunoglobulin E; allergy; atopy;
KW conjunctivitis; rhinitis; anaphylaxis; urticaria; angioedema.
XX
OS Homo sapiens.
XX
PN WO200121816-A1.
XX
PD 29-MAR-2001.
XX
PF 21-SEP-2000; 2000WO-US025877.
XX
PR 21-SEP-1999; 99US-0154924P.
XX
(ISIS-) ISIS INNOVATION LTD.
(BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
PI Kinet J, Donnadieu E, Jouvin M, Cookson W, Moffatt MF;
XX
WPI; 2001-266077/27.
XX
N-PSDB; AAF77689.
XX
PT Inhibiting expression of high affinity receptors for immunoglobulin (Ig)
PT E, in cell or in subject to treat atopy, anaphylaxis mediated by IGE, by
XX contacting cell or administering to subject, a FcERbeta chain variant.
XX
PS Claim 5; Page 51; 55pp; English.
XX
CC The present invention describes a method of inhibiting the expression of
CC the FcpsiIonRi receptor by contacting a cell expressing it with an
CC FcpsiIonRibeta chain variant. The FcpsiIonRi receptor is a high affinity
CC receptor for immunoglobulin E. The method is useful in the treatment of
CC allergic conditions such as rhinitis, conjunctivitis, atopy, anaphylaxis,
CC urticaria and angioedema. The present sequence is the variant human
XX FcpsiIonRibeta chain
XX
SQ Sequence 195 AA;

Query Match 100.0%; Score 1002; DB 4; Length 195;
Best Local Similarity 100.0%; Pred. No. 1.7e-105; Indels 0; Gaps 0;
Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDTESNRRANLALPOEPSSVPAFEVLEISPOEVSSGRLLKSSASSPPLHTWLTWLVKKEQEF 60
DB 1 MDTESNRRANLALPOEPSSVPAFEVLEISPOEVSSGRLLKSSASSPPLHTWLTWLVKKEQEF 60

QY 61 LGVTQILTAMICLCFGTVVCSVLDISHIEDIFSSPKAGYPPFWGAIFFPSISGMLSIISER 120
DB 61 LGVTQILTAMICLCFGTVVCSVLDISHIEDIFSSPKAGYPPFWGAIFFPSISGMLSIISER 120

QY 121 RNATYLVVRGSLGANTASSIAGGTITILINLKKSLAYIHHSCKQFFETKCFMASFSTV 180
DB 121 RNATYLVVRGSLGANTASSIAGGTITILINLKKSLAYIHHSCKQFFETKCFMASFSTV 180

QY 181 CFFFCVGRRLRFVWLM 195
DB 181 CFFFCVGRRLRFVWLM 195

RESULT 2
AAW29149
ID AAW29149 standard; protein; 244 AA.
XX
AC AAW29149;
XX
DT 12-DEC-1997 (first entry)
XX
DE Human high affinity IGE receptor beta chain E237G variant.
XX
KW human; immunoglobulin E; high affinity receptor; beta subunit; IGE;
KW Fc epsilon RI beta; exon 7; variant; E237G; atopy; atopic asthma;
KW detection; diagnosis; polymorphism; subgroup; clinical management.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 237 /note= "E237G variant"
FT
XX
PN WO9708338-A1.
XX
PD 06-MAR-1997.
XX
PF 29-AUG-1996; 96WO-GB002095.
XX
PR 29-AUG-1995; 95GB-00017585.
XX
PA (ISIS-) ISIS INNOVATIONS LTD.
XX
PI Cookson WOC, Hill MR;
XX
DR WPI; 1997-179293/16.
DR N-PSDB; AAT86756.
XX
PT Diagnosing atopy, or predisposition to it - by detection of
PT immunoglobulin E high affinity receptor beta subunit exon 7 variant
PT Glu237Gly.
XX
PS Disclosure; Page; 25pp; English.
XX
CC This is the human immunoglobulin E (IGE) high affinity receptor beta
CC subunit (Fc epsilon RI beta) exon 7 variant E237G. This variant is
CC associated with atopy and atopic asthma. The variation is in exon 7 (see
CC T86756) and is a nucleotide change from adenine to guanine at nucleotide
CC 7297 (nucleotide 6843 in the Fc epsilon RI beta gene sequence of Kuster,
CC et al. 1992). Detection of the protein is useful for diagnosis of asthma.
CC In particular the E237G polymorphism may also define a subgroup of asthma
CC sufferers with a particular clinical course, in which case recognition of
CC the variant/polymorphism would be of value in defining asthma prognosis
CC and management. NB. This sequence was created using the sequence given in
CC Genbank M89796

XX SQ Sequence 244 AA;
Query Match 90.8%; Score 910; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. No. 7.3e-95; Indels 0; Gaps 0;
Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDTESNRRANLALPOEPSSVPAFEVLEISPOEVSSGRLLKSSASSPPLHTWLTWLVKKEQEF 60
DB 1 MDTESNRRANLALPOEPSSVPAFEVLEISPOEVSSGRLLKSSASSPPLHTWLTWLVKKEQEF 60

QY 61 LGVTQILTAMICLCFGTVVCSVLDISHIEDIFSSPKAGYPPFWGAIFFPSISGMLSIISER 120
DB 61 LGVTQILTAMICLCFGTVVCSVLDISHIEDIFSSPKAGYPPFWGAIFFPSISGMLSIISER 120

QY 121 RNATYLVVRGSLGANTASSIAGGTITILINLKKSLAYIHHSCKQFFETKCFMASFST 179
DB 121 RNATYLVVRGSLGANTASSIAGGTITILINLKKSLAYIHHSCKQFFETKCFMASFST 179

RESULT 3
AAW75918
ID AAW75918 standard; protein; 244 AA.
XX
AC AAW75918;
XX
DT 13-NOV-1998 (first entry)
XX
DE Human beta subunit of Fc epsilon RI polypeptide sequence.
XX
KW Human beta subunit of Fc epsilon RI; ARAM; Fc epsilon RI beta chain;
KW antigen recognition activation motif; human beta subunit; allergy;
KW high-affinity immunoglobulin E receptor.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 60..80 /note= "transmembrane domain"
FT Domain 99..118 /note= "transmembrane domain"
FT Domain 129..150 /note= "transmembrane domain"
FT Domain 181..201 /note= "transmembrane domain"
FT
XX
PN US5807988-A.
XX
PD 15-SEP-1998.
XX
PF 24-FEB-1994; 94US-00201879.
XX
PR 16-APR-1992; 92US-00869933.
PR 16-APR-1993; 93WO-US003419.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Jouvin M, Kinet J;
XX
DR WPI; 1998-520207/44.
DR N-PSDB; AAV54661.
XX
PT Human IGE receptor beta subunit protein - and corresponding peptide(s)
PT and fusion protein.
XX
PS Claim 2; Col 43-44; 55pp; English.
XX
CC This represents the polypeptide sequence of a human beta subunit of Fc
CC epsilon RI [high-affinity immunoglobulin E receptor]. The invention
CC provides a peptide fragment (AAW75917) from the human Fc epsilon RI beta
CC subunit protein that contains the amino acid sequence of an ARAM (antigen
CC recognition activation motif). Aspects of the invention are methods and
CC compositions to inhibit the function of human beta subunit, thereby

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OM protein - protein search, using sw model

Run on: March 2, 2006, 18:45:16 ; Search time 21.7654 Seconds
(without alignments)
862.024 Million cell updates/sec

Title: US-10-088-703A-4

Perfect score: 1002
Sequence: 1 MDTESNRANLALPQPPSSV.....SFSTVCIFVCORLRFWVLM 195

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80.*

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	91.0	90.8	244	A42806	IgE Fc receptor beta
2	56.0	55.9	152	JH0751	IgE receptor beta
3	49.1	49.1	235	B34342	IgE Fc receptor beta
4	47.5	47.4	243	A31231	high-affinity IgE
5	15.3	15.3	214	I59258	IgE receptor beta
6	12.4	12.4	297	A30586	B-cell surface ant
7	11.3	11.3	200	JC7585	testis expressed t
8	10.3	10.3	291	A30558	B-cell surface ant
9	8.9	8.9	904	RDNTNT	nitrate reductase
10	85.5	8.5	1235	C69165	hypothetical prote
11	83.5	8.3	466	H81697	amino acid antipor
12	83.5	8.3	669	T08827	hypothetical prote
13	83.5	8.3	4447	A96679	polyketide synthas
14	81.5	8.1	377	G71341	conserved hypothet
15	81	8.1	891	RDHNPT	nitrate reductase
16	80	8.0	904	RDNTNS	nitrate reductase
17	80	8.0	921	E86764	conserved hypothet
18	79.5	7.9	449	G95876	probable permease
19	79.5	7.9	701	F70155	Na+/H+ antiporter
20	79	7.9	282	S26030	NADH2 dehydrogenas
21	78.5	7.8	659	E86313	hypothetical prote
22	77.5	7.7	362	C88086	protein Tif1.1 (i
23	77	7.7	358	C82281	ferric vibriobacti
24	77	7.7	387	A47287	estradiol 17beta-d
25	77	7.7	917	E96807	nitrate reductase
26	77	7.7	917	S35228	nitrate reductase
27	76.5	7.6	570	S07744	NADH2 dehydrogenas
28	76	7.6	125	D85595	probable membrane
29	76	7.6	125	H90744	probable membrane

30 76 7.6 125 2 H64822 probable membrane
31 76 7.6 229 2 S12593 nonstructural prot
32 76 7.6 463 2 T46290 hypothetical prote
33 76 7.6 764 2 A47456 down-regulated in
34 76 7.6 909 2 JN0665 nitrate reductase
35 76 7.6 1010 2 T33372 hypothetical prote
36 75.5 7.5 596 2 A46414 histidine protein
37 75.5 7.5 597 2 C87381 sensor histidine k
38 75.5 7.5 606 1 QXB05M NADH2 dehydrogenas
39 75.5 7.5 669 2 S64795 suppressor protein
40 75 7.5 230 1 A42949 cAMP receptor prot
41 75 7.5 258 2 G75372 conserved hypothet
42 75 7.5 449 2 JC5391 presenilin-beta -
43 75 7.5 584 2 D84264 hypothetical prote
44 75 7.5 1053 2 S72194 hydroxymethylgluta
45 75 7.5 4196 2 T43274 dynein heavy chain

ALIGNMENTS

RESULT 1
A42806
IgE Fc receptor beta chain - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 09-Jul-2004
C:Accession: A42806; S21154
R:Kuester, H.; Zhang, L.; Brini, A.T.; MacGlashan, D.W.J.; Kinet, J.P.
J. Biol. Chem. 267, 12782-12787, 1992
A:Title: The gene and cDNA for the human high affinity immunoglobulin E receptor beta
A:Reference number: A42806; MUID:92316966; PMID:1535625
A:Accession: A42806
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-244 <KUE>
A:Cross-references: UNIPROT:Q01362; UNIPARC:UPI0000038B6F; GB:M89796; NID:G337417; PII
R:Maekawa, K.; Imagawa, N.; Tanaka, Y.; Harada, S.
FEBS Lett. 302, 161-165, 1992
A:Title: Determination of the sequence coding for the beta subunit of the human high-a
A:Reference number: S21154; MUID:92339505; PMID:1386024
A:Accession: S21154
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-244 <MAE>
A:Cross-references: UNIPARC:UPI0000038B6F; GB:D10583; NID:G219881; PIDN:BAA0140.1; PI
C:Genetics: 19/2; 62/3; 107/3; 126/3; 179/3; 212/3
A:Introns: 19/2; 62/3; 107/3; 126/3; 179/3; 212/3
C:Keywords: immunoglobulin receptor; transmembrane protein
Query Match 90.8%; Score 910; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.4e-80; Mismatches 0; Indels 0; Gaps 0;
Matches 179; Conservative 0;

QY 1 MDTESNRANLALPQPPSSVPAFEVLEISPOQVSSGRLLKSASSPPLHTLTLVTKKEQF 60
Db 1 MDTESNRANLALPQPPSSVPAFEVLEISPOQVSSGRLLKSASSPPLHTLTLVTKKEQF 60
QY 61 LGVTOILTAMICLCFGTVCSVLDSHIEGDISSFKAGYPPWGAIFFSISGMLSIISER 120
Db 61 LGVTOILTAMICLCFGTVCSVLDSHIEGDISSFKAGYPPWGAIFFSISGMLSIISER 120
QY 121 RNATYLVKSGLCANTASSIAGTGTTILIIINLKKSLAYIIHSCOKFFETKCFMASFST 179
Db 121 RNATYLVKSGLCANTASSIAGTGTTILIIINLKKSLAYIIHSCOKFFETKCFMASFST 179

RESULT 2
JH0751
IgE receptor beta chain - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: JH0751
R:Bieber, T.; de la Salle, H.; Wollenberg, A.; Hakim, J.; Chizzonite, R.; Ring, J.; H

J. Exp. Med. 175, 1285-1290, 1992
A;Title: Human epidermal Langerhans cells express the high affinity receptor for immunoglobulin E; Keywords: Immunoglobulin receptor; transmembrane protein
A;Reference number: JH0751; MUID:92235608; PMID:1533242
A;Accession: JH0751
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-152 <BIE>
A;Cross-references: UNIPROT:Q14298; UNIPARC:UPI0000073ACE; GB:X66187; NID:g396463; PIDN:
Query Match 55.9%; Score 560; DB 2; Length 152;
Best Local Similarity 99.1%; Pred. No. 6.4e-47;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 71 ICLCFGTWVCSVLDSHIEGDISSFKAGYPPFWGAIFFSISGMLSIISERNATYLVRS 130
DB 1 ICLCFGTWVCSVLDSHIEGDISSFKAGYPPFWGAIFFSISGMLSIISERNATYLVRS 60
QY 131 LGANTASSIAGGTGTTILINLKSLAYIIHSCQKFFETKCPMASFST 179
DB 61 LGANTASSIAGGTGTTILINLKSLAYIIHSCQKFFETKCPMASFST 109
RESULT 3
B34342
IGE Fc receptor beta chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 09-Jul-2004
C;Accession: B34342
R;Ra, C.; Jouvin, M.H.E.; Kinet, J.P.
J. Biol. Chem. 264, 15323-15327, 1989
A;Title: Complete structure of the mouse mast cell receptor for IgE (Fc-epsilon-RI) and
A;Reference number: A34342; MUID:89359361; PMID:2527850
A;Accession: B34342
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-235 <RAC>
A;Cross-references: UNIPROT:P20490; UNIPARC:UPI00000223FC; GB:J05019; NID:g193238; PIDN:
C;Keywords: Immunoglobulin receptor; transmembrane protein
Query Match 49.1%; Score 492; DB 2; Length 235;
Best Local Similarity 52.3%; Pred. No. 4.2e-40;
Matches 103; Conservative 26; Mismatches 44; Indels 24; Gaps 5;
QY 1 MDTESNRANLAL--POEPSVPFAFEVLEISPOEVSSGRLLKASPPPLHTWTLTKKEQ 58
DB 1 MDTENSRADLALPNQESSAPDIELLEASP-----AKAAPPKQTWTFLLKEL 50
QY 59 EFLGVTOILTAMICLCFGTVVCSVLDSHIEGDISSFKAGYPPFWGAIFFSISGMLSIIS 118
DB 51 EFLGATQILVGLICLCFGTVVCSVLVSDPDEEVLLYKLGYPFWGAVFLVSGFLSIIS 110
QY 119 ERNATYLVRSGLANTASSIAGGTGTTILINLKSLAYIIHSCQKFFETK-CPMASF 177
DB 111 ERKNTLYLVRSGLANIVSSIAAGTGIFAMILNLNTNNFAY--MNNCKNVTEDDGCVFASF 168
QY 178 STVCIF-----FC 185
DB 169 TTELVMMLFLTLAFC 185
RESULT 4
A31231
high-affinity IGE receptor beta chain - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: A31231
R;Kinet, J.P.; Blank, U.; Ra, C.; White, K.; Metzger, H.; Kochan, J.
Proc. Natl. Acad. Sci. U.S.A. 85, 6483-6487, 1988
A;Title: Isolation and characterization of cDNAs coding for the beta-subunit of the high
A;Reference number: A31231; MUID:88320465; PMID:2970642
A;Accession: A31231
A;Molecule type: mRNA
A;Residues: 1-243 <KIN>

A;Cross-references: UNIPROT:PL3386; UNIPARC:UPI000003FF8D; GB:M22923; GB:J03845; NID:
C;Keywords: Immunoglobulin receptor; transmembrane protein
Query Match 47.4%; Score 475; DB 2; Length 243;
Best Local Similarity 51.8%; Pred. No. 1.9e-38;
Matches 102; Conservative 23; Mismatches 56; Indels 16; Gaps 5;
QY 1 MDTESNRANLAL--POEPSVPFAFEVLEISPOEVSSGRLLKASPPPLHTWTLTKKEQ 58
DB 1 MDTENSRADLALPNQESSAPDIELLEASPAPKALPE--KPASPPPOQTWQSFLLKEL 58
QY 59 EFLGVTOILTAMICLCFGTVVCSVLDSHIEGDISSFKAGYPPFWGAIFFSISGMLSIIS 118
DB 59 EFLGATQILVGLICLCFGTVVCSVLTSQTSDFDDEVLLYKLGYPFWGAVFLVSGFLSIIS 118
QY 119 ERNATYLVRSGLANTASSIAGGTGTTILINLKSLAYIIHSCQKFFETK-CPMASF 177
DB 111 ERKNTLYLVRSGLANIVSSIAAGTGIFAMILNLNNSAYMNY--CKDITEDDGCFTVSF 176
QY 178 STVCIF-----FC 185
DB 177 TTELVMMLFLTLAFC 193
RESULT 5
I59258
IGE receptor beta chain / CD20 antigen homolog - human
C;Species: Homo sapiens (man)
C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 05-Nov-1999
C;Accession: I59258
R;Adra, C.N.; Laliass, J.M.; Kobayashi, H.; Kaghad, M.; Morrison, P.; Rowley, J.D.; Lin
Proc. Natl. Acad. Sci. U.S.A. 91, 10178-10182, 1994
A;Title: Cloning of the cDNA for a hematopoietic cell-specific protein related to CD20
nning regions.
A;Reference number: I59258; MUID:95024008; PMID:7524084
A;Accession: I59258
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-214 <RES>
A;Cross-references: UNIPARC:UPI000002EF35; GB:L35848; NID:g561638; PIDN:AAA62319.1; PI
C;Genetics:
A;Gene: GDB:CD20L; HTM4
A;Cross-references: GDB:392702
A;Map position: 11q12-11q13.1
C;Keywords: Immunoglobulin receptor
Query Match 15.3%; Score 153; DB 2; Length 214;
Best Local Similarity 28.8%; Pred. No. 2.6e-07;
Matches 45; Conservative 26; Mismatches 73; Indels 12; Gaps 5;
QY 27 EISPOEVSSGRLLKASPPPLHTWTLTKKEQEFVLTQITLTMICLCFGTVVCSVLDS 86
DB 23 ETGPELNTSVYHPINGSPTYQ-----KAKQLVLGAIQILNAAITLALGVFLGSLQY 76
QY 87 HTEGD-IPSPKAGYPPFWGAIFFSISGMLSIISERNATYLVRSGLANTASSIAGGTGI 145
DB 77 HFQKHFFFTFTGTGTPINGAVFCCSGTILSVVAGIKPTFTWTQNSFGMIASATIALVGT 136
QY 146 TILINLKSLAYIIHSCQKFFETK--C-FMASFS 178
DB 137 AFLSLNIAVNIQ--SLRSCHSSSPDLCLNYMGSIS 170
RESULT 6
A30586
B-cell surface antigen CD20 - human
N;Alternate names: B-lymphocyte antigen CD20; B1
C;Species: Homo sapiens (man)
C;Date: 08-Jun-1989 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: A30586; J10042; A27400; S00387
R;Tedder, T.F.; Klejman, G.; Schlossman, S.F.; Saito, H.
J. Immunol. 142, 2560-2568, 1989
A;Title: Structure of the gene encoding the human B lymphocyte differentiation antigen

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OM protein - protein search, using sw model

Run on: March 2, 2006, 18:44:51 ; Search time 143.918 Seconds
(without alignments)
955.947 Million cell updates/sec

Title: US-10-088-703A-4
Perfect score: 1002
Sequence: 1 MDTENRRANLALPOEPSSV.....SFSTVCIFPCVGRLEFRWLM 195

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	910	90.8	244	1	FCERB_HUMAN	Q01362 homo sapien
2	910	90.8	244	2	Q5A81_HUMAN	Q5A81 homo sapien
3	560	55.9	152	2	Q14298_HUMAN	Q14298 homo sapien
4	492	49.1	235	1	FCERB_MOUSE	P20490 mus musculus
5	481.5	48.1	243	2	Q8WJ38_PIG	Q8WJ38 sus scrofa
6	475	47.4	243	1	FCERB_RAT	P13386 rattus norv
7	188.5	18.8	244	1	M4A6B_MOUSE	Q99N09 mus musculus
8	188.5	18.8	247	2	Q5XIJ0_RAT	Q5XIJ0 rattus norv
9	188.5	18.8	679	2	Q96J44_HUMAN	Q96J44 homo sapien
10	187.5	18.7	267	1	M4A8A_MOUSE	Q99N10 mus musculus
11	186.5	18.6	287	1	M4A8A_MOUSE	Q99N07 mus musculus
12	183	18.3	247	1	M4A6D_MOUSE	Q99N07 mus musculus
13	177	17.7	239	1	M4A4A_HUMAN	Q96J45 homo sapien
14	174.5	17.4	250	1	M4A8B_HUMAN	Q99J19 homo sapien
15	171	17.1	220	2	Q4JF27_HUMAN	Q4JF27 homo sapien
16	156.5	15.6	217	1	M4A6C_MOUSE	Q99N08 mus musculus
17	154.5	15.4	241	2	Q567K1_BRARE	Q567K1 brachydanio
18	154	15.4	214	1	MSA43_HUMAN	Q96J45 homo sapien
19	153	15.3	222	2	Q58DM5_BOVIN	Q58DM5 bos taurus
20	149.5	14.9	213	1	MSA43_MOUSE	Q920C4 mus musculus
21	149.5	14.9	213	2	Q810H7_MOUSE	Q810H7 mus musculus
22	149.5	14.9	213	2	Q53ZU3_MOUSE	Q53ZU3 mus musculus
23	149	14.9	205	2	Q8BL29_MOUSE	Q8BL29 mus musculus
24	149	14.9	234	2	Q99N04_MOUSE	Q99N04 mus musculus
25	146	14.6	267	2	Q8BV59_MOUSE	Q8BV59 mus musculus
26	145	14.5	234	2	Q8R3W1_MOUSE	Q8R3W1 mus musculus
27	144.5	14.4	197	2	Q810P8_MOUSE	Q810P8 mus musculus
28	143.5	14.3	240	1	MSA47_HUMAN	Q99Z88 homo sapien
29	143.5	14.3	240	2	Q61AG8_HUMAN	Q61AG8 homo sapien
30	142	14.2	298	2	Q5R1M8_FELCA	Q5R1M8 felis silve
31	138	13.8	248	1	M4A6A_HUMAN	Q9H2W1 homo sapien

32	135.5	13.5	252	2	Q567H8_BRARE	Q567H8 brachydanio
33	129.5	12.9	234	2	Q66ID5_BRARE	Q66ID5 brachydanio
34	129.5	12.9	1139	2	Q80WF0_RAT	Q80WF0 rattus norv
35	126.5	12.6	226	2	Q9D3F6_MOUSE	Q9D3F6 mus musculus
36	126	12.6	147	2	Q8NSU1_HUMAN	Q8NSU1 homo sapien
37	124	12.4	297	1	CD20_HUMAN	P11936 homo sapien
38	120	12.0	241	2	Q5BLB6_BRARE	Q5BLB6 brachydanio
39	120	12.0	267	1	M4A10_HUMAN	Q96J45 homo sapien
40	118.5	11.8	183	2	Q8C2D9_MOUSE	Q8C2D9 mus musculus
41	118.5	11.8	226	2	Q9ES61_MOUSE	Q9ES61 mus musculus
42	116	11.6	264	2	Q5REZ5_PONPY	Q5REZ5 pongo pygma
43	115	11.5	231	2	Q5M796_XENTR	Q5M796 xenopus tro
44	113.5	11.3	135	2	Q95LT4_MACFA	Q95LT4 macaca fasc
45	113.5	11.3	170	2	Q4R3P9_MACFA	Q4R3P9 macaca fasc

ALIGNMENTS

RESULT 1
FCERB_HUMAN
ID FCERB_HUMAN STANDARD; PRT; 244 AA.
AC Q01362;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DE High affinity immunoglobulin epsilon receptor beta-subunit (FcERI)
DE (Ige Fc receptor, beta-subunit) (Fc epsilon receptor I beta-chain).
GN Name=MS4A2; Synonyms=FCER1B, IGER;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92316966; PubMed=1535625;
RA Kuester H., Zhang L., Brini A.T., Macglashan D.W., Kinet J.-P.;
RT "The gene and cDNA for the human high affinity immunoglobulin E
receptor beta chain and expression of the complete human receptor.";
RL J. Biol. Chem. 267:12782-12787(1992).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=1386024; DOI=10.1016/0014-5793(92)80430-O;
RA Maekawa K., Imagawa N., Tanaka Y., Harada S.;
RT "Determination of the sequence coding for the beta subunit of the
human high-affinity Ige receptor.";
RL FEBS Lett. 302:161-165(1992).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
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Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield V.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 2, 2006, 18:46:52 ; Search time 16.4351 seconds
(without alignments)
980.936 Million cell updates/sec

Title: US-10-088-703A-4

Perfect score: 1002

Sequence: 1 MDTESNRRANLALPOEPSSV.....SFSTVCIFPCVGRRLRFWLM 195

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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- 3: /cgn2_6/prodata/1/iaa/H COMB.pep.*
- 4: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep.*
- 5: /cgn2_6/prodata/1/iaa/RE COMB.pep.*
- 6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	910	90.8	244	1	US-07-869-933-32
2	910	90.8	244	1	US-08-201-879A-3
3	910	90.8	244	2	US-09-103-663-32
4	910	90.8	244	2	US-09-949-016-5892
5	910	90.8	256	2	US-09-949-016-8329
6	492	49.1	235	1	US-07-869-933-34
7	492	49.1	235	1	US-08-201-879A-5
8	492	49.1	235	2	US-09-103-663-34
9	475	47.4	243	1	US-07-869-933-29
10	475	47.4	243	1	US-07-869-933-33
11	475	47.4	243	1	US-08-201-879A-4
12	475	47.4	243	1	US-08-916-902A-4
13	475	47.4	243	1	US-09-213-389-4
14	475	47.4	243	2	US-09-103-663-29
15	475	47.4	243	2	US-09-103-663-33
16	475	47.4	246	1	US-07-869-933-23
17	475	47.4	246	2	US-09-103-663-23
18	187.5	18.7	299	2	US-09-904-615-73
19	187.5	18.7	299	2	US-10-054-988-73
20	182	18.2	247	2	US-09-724-864-49
21	181.5	18.1	307	2	US-09-904-615-142
22	181.5	18.1	307	2	US-10-054-988-142
23	177	17.7	239	1	US-08-916-902A-1
24	177	17.7	239	1	US-09-213-389-1
25	177	17.7	239	2	US-10-164-595-74
26	174.5	17.4	250	2	US-09-702-705-1677
27	174.5	17.4	250	2	US-09-736-457-1677

28	174.5	17.4	250	2	US-09-671-325-1677	Sequence 1677, Ap
29	174.5	17.4	250	2	US-09-658-824-1677	Sequence 1677, Ap
30	174.5	17.4	250	2	US-10-017-754-1677	Sequence 1677, Ap
31	174.5	17.4	250	2	US-10-017-754-2004	Sequence 2004, Ap
32	174.5	17.4	250	2	US-09-651-563-1677	Sequence 1677, Ap
33	166.5	16.6	250	2	US-10-017-754-1874	Sequence 1874, Ap
34	166.5	16.6	286	2	US-10-017-754-1876	Sequence 1876, Ap
35	166.5	16.6	384	2	US-10-017-754-1876	Sequence 1876, Ap
36	153	15.3	214	1	US-08-318-492-4	Sequence 4, Appli
37	153	15.3	214	1	US-08-707-340-4	Sequence 4, Appli
38	153	15.3	214	1	US-08-916-902A-3	Sequence 3, Appli
39	153	15.3	214	1	US-08-994-578-4	Sequence 4, Appli
40	153	15.3	214	1	US-09-213-389-3	Sequence 3, Appli
41	142	14.2	204	2	US-09-904-615-117	Sequence 117, App
42	142	14.2	204	2	US-10-054-988-117	Sequence 117, App
43	138	13.8	225	2	US-09-855-323-14	Sequence 14, Appl
44	138	13.8	242	2	US-09-311-021-212	Sequence 212, App
45	138	13.8	248	2	US-09-489-847-207	Sequence 207, App

ALIGNMENTS

RESULT 1
US-07-869-933-32
; Sequence 32, Application US/07869933
; Patent No. 5770396
; GENERAL INFORMATION:
; APPLICANT: KINET, Jean-Pierre
; TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
; TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/869,933
; FILING DATE: 19920416
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 40399/154 NIHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 244 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; STRAIN: FcR1 beta subunit
; US-07-869-933-32

Query Match 90.8%; Score 910; DB 1; Length 244;
Best Local Similarity 100.0%; Pred. No. 2e-102;
Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 LGVTOILTAMICLCFGTVVCSVLDSHIEGDISSFKAGYPPFWGAIFFSISGMLSIISER 120
Db 61 LGVTOILTAMICLCFGTVVCSVLDSHIEGDISSFKAGYPPFWGAIFFSISGMLSIISER 120
QY 121 RNATYLRGSLGANTASSIAGGTGTTILINLKSLAYIHHSCKQFFETKCFMASFST 179
Db 121 RNATYLRGSLGANTASSIAGGTGTTILINLKSLAYIHHSCKQFFETKCFMASFST 179

RESULT 2

US-08-201-879A-3
; Sequence 3, Application US/08201879A
; Patent No. 5807988
; GENERAL INFORMATION:
; APPLICANT: KINET, Jean-Pierre
; APPLICANT: JOUVIN, Marie-Helene
; TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
; TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
; TITLE OF INVENTION: IMMUNOGLOBULIN E
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/201,879A
; FILING DATE: 24-FEB-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/869,933
; FILING DATE: 16-APR-1992
; PRIOR APPLICATION DATA: PCT/US93/03419
; FILING DATE: 16-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 40399/234/NIHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 244 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-201-879A-3

Query Match 90.8%; Score 910; DB 1; Length 244;
Best Local Similarity 100.0%; Pred. No. 2e-102;
Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 61 LGVTOILTAMICLCFGTVVCSVLDSHIEGDISSFKAGYPPFWGAIFFSISGMLSIISER 120

QY 121 RNATYLRGSLGANTASSIAGGTGTTILINLKSLAYIHHSCKQFFETKCFMASFST 179
Db 121 RNATYLRGSLGANTASSIAGGTGTTILINLKSLAYIHHSCKQFFETKCFMASFST 179

RESULT 3

US-09-103-663-32
; Sequence 32, Application US/09103663D
; Patent No. 6171803
; GENERAL INFORMATION:
; APPLICANT: Kinet et al.
; TITLE OF INVENTION: Isolation, characterization, and use of the human beta
; TITLE OF INVENTION: subunit of the high affinity receptor for
; TITLE OF INVENTION: immunoglobulin E.
; FILE REFERENCE: 50490
; CURRENT APPLICATION NUMBER: US/09/103,663D
; EARLIER FILING DATE: 1998-06-23
; EARLIER APPLICATION NUMBER: 07/869,933
; EARLIER FILING DATE: 1992-04-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent-in-Ver. 2.1
; SEQ ID NO 32
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-103-663-32

Query Match 90.8%; Score 910; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. No. 2e-102;
Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MDTESNRNALALPOEPPSSVPAFEVLEISPOEVSSGRLLKASASPPLHTLWTLVKKEQEF 60
QY 61 LGVTOILTAMICLCFGTVVCSVLDSHIEGDISSFKAGYPPFWGAIFFSISGMLSIISER 120
Db 61 LGVTOILTAMICLCFGTVVCSVLDSHIEGDISSFKAGYPPFWGAIFFSISGMLSIISER 120
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Db 121 RNATYLRGSLGANTASSIAGGTGTTILINLKSLAYIHHSCKQFFETKCFMASFST 179

RESULT 4

US-09-949-016-5892
; Sequence 5892, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5892
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-5892

Query Match 90.8%; Score 910; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. No. 2e-102;
Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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5	475	47.4	243	4	US-10-433-287-52
6	188.5	18.8	244	4	US-10-433-287-28
7	187.5	18.7	244	3	US-09-981-353-82
8	187.5	18.7	273	5	US-10-450-763-47363
9	187.5	18.7	299	3	US-09-739-254-73
10	187.5	18.7	299	3	US-09-304-615-73
11	187.5	18.7	299	4	US-10-054-988-73
12	186.5	18.6	268	4	US-10-433-287-36
13	184	18.4	267	4	US-10-433-287-46
14	183	18.3	247	4	US-10-433-287-32
15	182.5	18.2	240	5	US-10-484-148-7
16	182	18.2	247	3	US-09-866-050A-687
17	181.5	18.1	307	3	US-09-739-254-142
18	181.5	18.1	307	3	US-09-904-615-142
19	181.5	18.1	307	4	US-10-054-988-142
20	178	17.8	197	4	US-10-295-027-452
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24	177	17.7	220	4	US-10-433-287-2
25	177	17.7	239	4	US-10-015-115-101
26	177	17.7	239	4	US-10-015-115-102
27	177	17.7	239	5	US-10-717-665-74

28	177	17.7	245	3	US-09-374-046A-152	Sequence 152, App
29	177	17.7	245	3	US-10-616-263-152	Sequence 152, App
30	174.5	17.4	250	4	US-09-736-457-1677	Sequence 1677, App
31	174.5	17.4	250	3	US-09-902-941-1677	Sequence 1677, App
32	174.5	17.4	250	3	US-09-849-626-1677	Sequence 1677, App
33	174.5	17.4	250	4	US-10-017-754-1677	Sequence 1677, App
34	174.5	17.4	250	4	US-10-017-754-2004	Sequence 2004, App
35	174.5	17.4	250	4	US-10-156-136-21	Sequence 21, Appl
36	174.5	17.4	250	4	US-10-113-872-1677	Sequence 1677, App
37	174.5	17.4	250	4	US-10-113-872-2004	Sequence 2004, App
38	174.5	17.4	250	4	US-10-283-017-1677	Sequence 1677, App
39	174.5	17.4	250	4	US-10-283-017-2004	Sequence 2004, App
40	174.5	17.4	250	4	US-10-295-027-624	Sequence 624, App
41	174.5	17.4	250	4	US-10-264-237-2566	Sequence 2566, App
42	174.5	17.4	250	4	US-10-433-287-16	Sequence 16, Appl
43	174.5	17.4	250	6	US-11-041-419-21	Sequence 21, Appl
44	174.5	17.4	302	3	US-09-925-297-764	Sequence 764, App
45	169.5	16.9	227	5	US-10-450-763-49595	Sequence 49595, A

ALIGNMENTS

RESULT 1
 US-10-369-214-124
 ; Sequence 124, Application US/10369214
 ; Publication No. US20030232037A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Groot, Pieter C.
 ; APPLICANT: Berghenhegouwen van, Bram J.
 ; APPLICANT: Oosterhout van, Antoon J.M.
 ; TITLE OF INVENTION: Genes involved in immune related responses observed
 ; TITLE OF INVENTION: with asthma
 ; FILE REFERENCE: P53837US00
 ; CURRENT APPLICATION NUMBER: US/10/369,214
 ; CURRENT FILING DATE: 2003-02-15
 ; PRIOR APPLICATION NUMBER: EP 00202867.8
 ; PRIOR FILING DATE: 2000-08-16
 ; PRIOR APPLICATION NUMBER: PCT/NL01/00610
 ; PRIOR FILING DATE: 2001-08-16
 ; NUMBER OF SEQ ID NOS: 139
 ; SOFTWARE: Patent in Ver. 2.1
 ; SEQ ID NO 124
 ; LENGTH: 244
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (1)..(244)
 ; OTHER INFORMATION: /note="Ige receptor beta chain"
 US-10-369-214-124
 Query Match 90.8%; Score 910; DB 4; Length 244;
 Best Local Similarity 100.0%; Pred. No. 6.3e+90;
 Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDTESNRRANLALPQBPSVPAFEVLEISPOQVSSGRLLKSASSPPLHTLWTLVTKKEQEF 60
 Db 1 MDTESNRRANLALPQBPSVPAFEVLEISPOQVSSGRLLKSASSPPLHTLWTLVTKKEQEF 60
 QY 61 LGVTQILTAMICLCFGTVVCSVLDISHIEGDIFFSFKAGYFPWGAIFFSISGMLSIISER 120
 Db 61 LGVTQILTAMICLCFGTVVCSVLDISHIEGDIFFSFKAGYFPWGAIFFSISGMLSIISER 120
 QY 121 RNATYLVGRSLGANTASSIAGTGTTILINLKSLAYIHHSCKQFFETKCFMASFST 179
 Db 121 RNATYLVGRSLGANTASSIAGTGTTILINLKSLAYIHHSCKQFFETKCFMASFST 179
 RESULT 2
 US-10-433-287-42
 ; Sequence 42, Application US/10433287
 ; Publication No. US20040137566A1

```
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F
; APPLICANT: Liang, Yinghua
; TITLE OF INVENTION: Identification of Novel Gene Family Members Expressed by
; TITLE OF INVENTION: Hematopoietic Cells
; FILE REFERENCE: 180/132 PCT/US
; CURRENT APPLICATION NUMBER: US/10/433,287
; CURRENT FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 42
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-433-287-42

Query Match          90.1%; Score 910; DB 4; Length 244;
Best Local Similarity 100.0%; Pred. No. 6.3e-90;
Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDTESNRANLALPOEPSSVPAPEVLEISPOEVSSGRLLKSASPPHLTWTVLKKEQEF 60
Db 1 MDTESNRANLALPOEPSSVPAPEVLEISPOEVSSGRLLKSASPPHLTWTVLKKEQEF 60
QY 61 LGVTQILTAMICLCFGTVVCSVLDISHIEGDISSFKAGYPPFWGAIFFSISGMLSIISER 120
Db 61 LGVTQILTAMICLCFGTVVCSVLDISHIEGDISSFKAGYPPFWGAIFFSISGMLSIISER 120
QY 121 RNATYLVRSGLGANTASSIAGGTGTTILINLKKSLAYIHSCQKFFETKCFMASFST 179
Db 121 RNATYLVRSGLGANTASSIAGGTGTTILINLKKSLAYIHSCQKFFETKCFMASFST 179

RESULT 3
US-10-369-214-123
; Sequence 123, Application US/10369214
; Publication No. US20030232037A1
; GENERAL INFORMATION:
; APPLICANT: Groot, Pieter C.
; APPLICANT: Bergenhegouwen van, Bram J.
; APPLICANT: Oosterhout van, Antoon J.M.
; TITLE OF INVENTION: Genes involved in immune related responses observed
; TITLE OF INVENTION: with asthma
; FILE REFERENCE: P53837US00
; CURRENT APPLICATION NUMBER: US/10/369,214
; CURRENT FILING DATE: 2003-02-15
; PRIOR APPLICATION NUMBER: EP 00202867.8
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: PCT/NL01/00610
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 123
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(235)
; OTHER INFORMATION: /note="Ige receptor beta chain"
; US-10-369-214-123

Query Match          49.1%; Score 492; DB 4; Length 235;
Best Local Similarity 52.3%; Pred. No. 1.3e-44;
Matches 103; Conservative 26; Mismatches 44; Indels 24; Gaps 5;

QY 1 MDTESNRANLALPOEPSSVPAPEVLEISPOEVSSGRLLKSASPPHLTWTVLKKEQ 58
Db 1 MDTESNRANLALPNQESSAPDIELLEASP-----AKAAPKQTWTFLKKEL 50
QY 59 EFLGVTQILTAMICLCFGTVVCSVLDISHIEGDISSFKAGYPPFWGAIFFSISGMLSIIS 118
Db 51 EFLGATQILVGLICLCFGTVVCSVLYVSDPEVLLLYKLYGYPFWGAVLVLSGFLSIIS 110
QY 119 ERNATYLVRSGLGANTASSIAGGTGTTILINLKKSLAYIHSCQKFFETK-CFMASF 177
Db 111 ERNATYLVRSGLGANIVSSIAAGTGIAMLINLTNNFAY--MNNCKNVTEDDGCFCVASF 168

Query Match          47.4%; Score 475; DB 4; Length 243;
Best Local Similarity 51.8%; Pred. No. 9.4e-43;
Matches 103; Conservative 26; Mismatches 44; Indels 24; Gaps 5;
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QY 119 ERNATYLVRSGLGANTASSIAGGTGTTILINLKKSLAYIHSCQKFFETK-CFMASF 177
Db 111 ERNATYLVRSGLGANIVSSIAAGTGIAMLINLTNNFAY--MNNCKNVTEDDGCFCVASF 168
QY 178 STVCIF-----FC 185
Db 169 TTTELVLMLFLTLAFC 185

RESULT 4
US-10-433-287-50
; Sequence 50, Application US/10433287
; Publication No. US20040137566A1
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F
; APPLICANT: Liang, Yinghua
; TITLE OF INVENTION: Identification of Novel Gene Family Members Expressed by
; TITLE OF INVENTION: Hematopoietic Cells
; FILE REFERENCE: 180/132 PCT/US
; CURRENT APPLICATION NUMBER: US/10/433,287
; CURRENT FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 50
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-433-287-50

Query Match          49.1%; Score 492; DB 4; Length 235;
Best Local Similarity 52.3%; Pred. No. 1.3e-44;
Matches 103; Conservative 26; Mismatches 44; Indels 24; Gaps 5;

QY 1 MDTESNRANLALPOEPSSVPAPEVLEISPOEVSSGRLLKSASPPHLTWTVLKKEQ 58
Db 1 MDTESNRANLALPNQESSAPDIELLEASP-----AKAAPKQTWTFLKKEL 50
QY 59 EFLGVTQILTAMICLCFGTVVCSVLDISHIEGDISSFKAGYPPFWGAIFFSISGMLSIIS 118
Db 51 EFLGATQILVGLICLCFGTVVCSVLYVSDPEVLLLYKLYGYPFWGAVLVLSGFLSIIS 110
QY 119 ERNATYLVRSGLGANTASSIAGGTGTTILINLKKSLAYIHSCQKFFETK-CFMASF 177
Db 111 ERNATYLVRSGLGANIVSSIAAGTGIAMLINLTNNFAY--MNNCKNVTEDDGCFCVASF 168
QY 178 STVCIF-----FC 185
Db 169 TTTELVLMLFLTLAFC 185

RESULT 5
US-10-433-287-52
; Sequence 52, Application US/10433287
; Publication No. US20040137566A1
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F
; APPLICANT: Liang, Yinghua
; TITLE OF INVENTION: Identification of Novel Gene Family Members Expressed by
; TITLE OF INVENTION: Hematopoietic Cells
; FILE REFERENCE: 180/132 PCT/US
; CURRENT APPLICATION NUMBER: US/10/433,287
; CURRENT FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 52
; LENGTH: 243
; TYPE: PRT
; ORGANISM: rat
; US-10-433-287-52

Query Match          47.4%; Score 475; DB 4; Length 243;
Best Local Similarity 51.8%; Pred. No. 9.4e-43;
Matches 103; Conservative 26; Mismatches 44; Indels 24; Gaps 5;
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 2, 2006, 18:51:46 ; Search time 7.55125 Seconds
(without alignments)
516.474 Million cell updates/sec

Title: US-10-088-703A-4
Perfect score: 1002
Sequence: 1 MDTESNRANLALPQBPSSV.....SFSTVCIFPCVGRLARFWLVM 195

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 135339 seqs, 20000136 residues

Total number of hits satisfying chosen parameters: 135339

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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3: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep.*
5: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pep.*
6: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep.*
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8: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	184	18.4	267	6	US-10-506-443A-38
2	143.5	14.3	297	7	US-11-138-949-6
3	142	14.2	298	7	US-11-138-949-9
4	124.5	12.4	297	7	US-11-190-364-25
5	124.5	12.4	297	7	US-11-147-780-25
6	124	12.4	297	7	US-11-138-949-7
7	124	12.4	297	7	US-11-190-364-26
8	124	12.4	297	7	US-11-147-780-26
9	118	11.8	248	5	US-09-578-360A-610
10	113	11.3	199	7	US-11-179-018-2
11	103.5	10.3	291	7	US-11-138-949-8
12	100	10.0	138	7	US-11-179-018-6
13	99.5	9.9	149	7	US-11-179-018-8
14	83.5	8.3	230	7	US-11-072-512-3554
15	77	7.7	394	6	US-10-821-234-1194
16	75	7.5	509	7	US-11-098-686-10325
17	74	7.4	172	7	US-11-036-797-36
18	72.5	7.2	5712	7	US-11-143-980-47
19	71.5	7.1	345	7	US-11-174-816-44
20	71.5	7.1	345	7	US-11-174-819-13
21	71.5	7.1	473	7	US-11-098-686-10759
22	71	7.1	538	7	US-11-119-683-1
23	71	7.1	801	6	US-10-453-372-468
24	70.5	7.0	7968	7	US-11-143-980-49
25	70	7.0	162	6	US-10-467-657-5624

26	70	7.0	437	7	US-11-087-099-6210	Sequence 6210, Ap
27	70	7.0	608	7	US-11-167-856-12	Sequence 12, Appl
28	70	7.0	843	6	US-10-645-441-7	Sequence 7, Appl
29	70	7.0	843	6	US-10-725-475-17	Sequence 17, Appl
30	69.5	6.9	633	6	US-10-912-580-7	Sequence 7, Appl
31	69.5	6.9	633	6	US-10-912-582-1	Sequence 1, Appl
32	69.5	6.9	882	6	US-10-912-580-8	Sequence 8, Appl
33	69.5	6.9	882	6	US-10-912-582-2	Sequence 2, Appl
34	69.5	6.9	882	7	US-11-050-857-95	Sequence 95, Appl
35	69	6.9	452	6	US-10-793-626-1834	Sequence 1834, Ap
36	69	6.9	463	7	US-11-087-099-5015	Sequence 5015, Ap
37	68.5	6.8	318	7	US-11-000-463-331	Sequence 331, App
38	68.5	6.8	318	7	US-11-000-463-803	Sequence 803, App
39	68.5	6.8	345	7	US-11-210-316-14	Sequence 14, Appl
40	68.5	6.8	594	7	US-11-087-099-1541	Sequence 1541, Ap
41	68.5	6.8	634	7	US-11-124-367A-285	Sequence 285, App
42	68	6.8	433	7	US-11-087-099-2288	Sequence 2288, Ap
43	68	6.8	506	7	US-11-013-592-8	Sequence 8, Appl
44	68	6.8	901	7	US-11-050-857-963	Sequence 963, App
45	67.5	6.7	966	7	US-11-087-099-11674	Sequence 11674, A

ALIGNMENTS

RESULT 1
US-10-506-443A-38
; Sequence 38, Application US/10506443A
; Publication No. US20060013817A1
; GENERAL INFORMATION:
; APPLICANT: Sahin Dr., Ugur
; APPLICANT: Tureci Dr., Ozlem
; APPLICANT: Koslowski Dr., Michael
; TITLE OF INVENTION: Genetic Products Differentially Expressed in Tumors and Use The
; FILE REFERENCE: 342-3PCT
; CURRENT APPLICATION NUMBER: US/10/506,443A
; CURRENT FILING DATE: 2004-09-01
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-506-443A-38

Query Match 18.4%; Score 184; DB 6; Length 267;
Best Local Similarity 30.9%; Pred. No. 3.5e-12;
Matches 47; Conservative 29; Mismatches 58; Indels 18; Gaps 3;

QY	44	SPPLHTWLTVLKKEQFLGVTOILTAMICLCFGTVVCSV-LDISHIEGDIFFSFKAGYPP	102
DB	74	NPSVGTAVNFKKEAKALGVIOIMVGLMHIGFVLCILISFSPFREVLFVGFSTAVIGGYPP	133
QY	103	WGAIFFSTGMLSIISERRNATYLVRSIGANTASSIAGGTGTTIILNL-----	152
DB	134	WGGISFIISGSLSVASAKLSCLVKGLMNVSSILAFIVGILLVDMCINGVAGODY	193
QY	153	-----KSLAVIHHSCKPFTKCFMASES	178
DB	194	WAVLSGKGISATLMIFSLLEFF-VACATAHFA	224

RESULT 2
US-11-138-949-6
; Sequence 6, Application US/11138949
; Publication No. US20050271662A1
; GENERAL INFORMATION:
; APPLICANT: Beall, Melissa J
; TITLE OF INVENTION: CANINE CD20 COMPOSITIONS
; FILE REFERENCE: 04-457A
; CURRENT APPLICATION NUMBER: US/11/138,949
; CURRENT FILING DATE: 2005-05-26
; PRIOR APPLICATION NUMBER: 60/575172

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; PRIOR FILING DATE: 2004-05-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 6
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Canis familiaris
US-11-138-949-6

Query Match      14.3%; Score 143.5; DB 7; Length 297;
Best Local Similarity 24.3%; Pred. No. 8.7e-08;
Matches 45; Conservative 33; Mismatches 58; Indels 39; Gaps 7;

QY 1 MDTESRRANALPOEPSSVPA--FEVLEISPOEVSSGRLLKASPPHLTWTVLKKEQF 58
Db 1 MTTPRNSMSG-TLPVDMKSPATAMPVQKIIPK-----MPSVVGPTQNFPM-----RES 49
QY 59 EFLGVTOILTAMICLCFGTVVCSVLDSHIEGDIFFS--SPKAGYPPFWGAIFPFSISGMLSI 116
Db 50 KTLGAVQIMNGLFHIALGSLM-----IHTDVIAPICITWVYPLWGGIMFIISGSLLA 102
QY 117 ISERNATYLRGSLGANTASSIAGGTGITILIN-----LKKSLAYI 159
Db 103 AADKNPKSLVKGKMINSLSLFAAISGIIFLIMDIENITISHFLKMNENLIKAPIYV 162
QY 160 HIHSC 164
Db 163 DIHNC 167

RESULT 3
US-11-138-949-9
; Sequence 9, Application US/11138949
; Publication No. US20050271662A1
; GENERAL INFORMATION:
; APPLICANT: Beall, Melissa J
; TITLE OF INVENTION: CANINE CD20 COMPOSITIONS
; FILE REFERENCE: 04-457A
; CURRENT APPLICATION NUMBER: US/11/138,949
; PRIOR FILING DATE: 2005-05-26
; PRIOR APPLICATION NUMBER: 60/575172
; PRIOR FILING DATE: 2004-05-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 9
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Felis catus
US-11-138-949-9

Query Match      14.2%; Score 142; DB 7; Length 298;
Best Local Similarity 22.8%; Pred. No. 1.3e-07;
Matches 49; Conservative 39; Mismatches 81; Indels 46; Gaps 7;

QY 1 MDTESRRANALPOEPSSVPAFEVLEISPOEVSSGRLLKASPPHLTWTVLKKEQF 60
Db 1 MTTPRNSMSG-TLPADAMKSP-----AMNPFVQKIIPKMPSVVGPTQNFPM-----RESK 51
QY 61 LGVTOILTAMICLCFGTVVCSVLDSHIEGDIFFSPKAGYPPFWGAIFPFSISGMLSIISER 120
Db 52 LGAVQIMNGLFHIALGSL-----MIHVEYAPICITWVYPLWGGIMFIISGSLLAEEK 106
QY 121 RNATYLRGSLGANTASSIAGGTGITILIN-----LKKSLAYIHIHS 163
Db 107 NPKSLVKGKMINSLSLFAAISGMILLIMDIENITISHFFKMNENLLKSPKPYDIHT 166
QY 164 CO-----KPFET--KCFMASPSTVCIF 183
Db 167 CQESKPEKSNLSIKYCDIRSIVFLSIFAMVVF 201

RESULT 4
US-11-190-364-25

; Sequence 25, Application US/11190364
; Publication No. US20060024300A1
; GENERAL INFORMATION:
; APPLICANT: Adams ET AL.
; TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof
; FILE REFERENCE: P1990R3C1P1
; CURRENT APPLICATION NUMBER: US/11/190,364
; PRIOR FILING DATE: 2005-07-26
; PRIOR APPLICATION NUMBER: US 60/434,115
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 60/526,163
; PRIOR FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: PCT/US03/40426
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 11/147,780
; PRIOR FILING DATE: 2005-06-07
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 25
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Macaca fascicularis
US-11-190-364-25

Query Match      12.4%; Score 124.5; DB 7; Length 297;
Best Local Similarity 24.3%; Pred. No. 9.3e-06;
Matches 42; Conservative 30; Mismatches 74; Indels 27; Gaps 6;

QY 3 TESNRRANALPOEPSSVPAFEVLEISPOEVSSGRLLKASPPHLTWTVLKKEQF 62
Db 2 TTPRNSVNGTTPAEPKMGK-----IAMQPGPKPLLRMSLVGPTQSFPM-----RESKALG 53
QY 63 VTQILTAMICLCFGTVVCSVLDSHIEGDIFFS--KAGYPPFWGAIFPFSISGMLSIISER 120
Db 54 AVQIMNGLFHIALGGLM-----IPAGIYAPICITWVYPLWGGIMFIISGSLLAATEK 106
QY 121 RNATYLRGSLGANTASSIAGGTGITILIN-----LKKSLAYIHIHS 163
Db 107 NSRKCLVKGKMINSLSLFAAISGMILSIMDIENITISHFLKMNENLNFIRVHT 159

RESULT 5
US-11-147-780-25
; Sequence 25, Application US/11147780
; Publication No. US20060034835A1
; GENERAL INFORMATION:
; APPLICANT: Adams ET AL.
; TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof
; FILE REFERENCE: P1990R3C1
; CURRENT APPLICATION NUMBER: US/11/147,780
; PRIOR FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US 60/434,115
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 60/526,163
; PRIOR FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: PCT/US03/40426
; PRIOR FILING DATE: 2003-12-16
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 25
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Macaca fascicularis
US-11-147-780-25

Query Match      12.4%; Score 124.5; DB 7; Length 297;
Best Local Similarity 24.3%; Pred. No. 9.3e-06;
Matches 42; Conservative 30; Mismatches 74; Indels 27; Gaps 6;

QY 3 TESNRRANALPOEPSSVPAFEVLEISPOEVSSGRLLKASPPHLTWTVLKKEQF 62
Db 2 TTPRNSVNGTTPAEPKMGK-----IAMQPGPKPLLRMSLVGPTQSFPM-----RESKALG 53
QY 63 VTQILTAMICLCFGTVVCSVLDSHIEGDIFFS--KAGYPPFWGAIFPFSISGMLSIISER 120
Db 54 AVQIMNGLFHIALGGLM-----IPAGIYAPICITWVYPLWGGIMFIISGSLLAATEK 106
QY 121 RNATYLRGSLGANTASSIAGGTGITILIN-----LKKSLAYIHIHS 163
Db 107 NSRKCLVKGKMINSLSLFAAISGMILSIMDIENITISHFLKMNENLNFIRVHT 159
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